Access D8# 98760

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Art Unit Phone Numb		Examiner # :	Date:
Art Unit. Phone Numb Mail Box and Bldg:Room Location:	per 30	Serial Number:	PAPER DISK F.MAI
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f more than one search is submitted			
Please provide a detailed statement of the search include the elected species or structures, keywo atility of the invention. Define any terms that n known. Please attach a copy of the cover sheet,	rds, synonyms, acron nay have a special me	yms, and registry numbers, and caning. Give examples or relevan	combine with the concept or
Title of Invention:			
Inventors (please provide full names):			
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Earliest Priority Filing Date:			
For Sequence Searches Only Please include all			patent numbers) along with the
appropriate serial number.			
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seq length: 0 seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                    July 15,
                                                                                      283224 seqs, 96134422 residues
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                                                                                                                                                                                                                                              2003, 06:52:29; Search time 13.4523 Seconds (without alignments)
1657.949 Million cell updates/sec
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Database PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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353	353	357	366.5	542	547	549	669	731.5	735	746.5	747.5	751.5	761	771	772	
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455	343	549	572	152	218	249	180	475	327	405	322	474	446	399	335	
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Ig mu chain C regi	Ig mu chain C regi	Ig heavy chain pre	Ig Y heavy chain (Ig gamma-1 chain C	Ig heavy chain V-I	Ig heavy chain VHI	Ig gamma heavy cha		· Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	

ALIGNMENTS

A; Accession: A90564 A; Accession: A90564 A; Molecule type: protein A; Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2 A; Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met R; Ponstingl, H.; Hilschmann, N. R; Ponstingl, H.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976 A; Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni	A; Molecule type: protein A; Molecule type: protein A; Residues: 1-96, 'R', 98-135 <cun> A; Residues: 1-96, 'R', 98-135 <cun> A; Note: this sequence has the Glm(3) marker, 97-Arg R; Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M. Biochemistry 9, 3171-3181, 1970 A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se A; Contents: Eu A; Contents: Eu</cun></cun>	A; Molecule type: DNA A; Residues: 88-113;235-330 <tak> A; Residues: 88-113;235-330 <tak> A; Residues: 88-113;235-330 <tak> A; Coss-references: EMBL:217370 R; Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma Biochemistry 9, 3161-3170, 1970 A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq A; Reference number: A90563; MUID:71064024; PMID:5489771 A; Contents: myeloma protein Eu A; Accession: B90563</tak></tak></tak>	17370 Obata, M.; Nikaio obata, M.; Nikaio n immunoglobulin n MUID:83001943;	RESULT 1 GHHU If gamma-1 chain C region - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999 C; Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146 R; Ellison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res 10, 4071-4079, 1982 A; Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A; Reference number: A93433; MUID:82274238; PMID:6287432 A; Accession: A93433 A; Molecule type: DNA A; Residues: 1-330 <ell> A; Note: this sequences: EMBL:Z17370 A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker A; Harris, L.J. submitted to the EMBL Data Library, October 1992</ell>	

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igen Primaerstruktur.
A; Reference number: A
A; Contents: myeloma p
A; Accession: B91668
                      Ig heavy chain V region precursor - hun (Species: Homo sapiens (man) C:Date: 19-Mar-11997 #sequence_revision C:Accession: S69339; 572664 R;Khamlichi, A.A.; Aucouturier, P.; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Complex: An immunoglobulin heterotetramer subunit consists of two ide hain disulfide bonds. In some cases, such as IgA and IgM, the subunits C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Keywords: immunoglobulin homology <IMI>
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A;Title: The covalent structure of a human gammaG-immunoglo A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1349, 1570-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-1649, 1571-
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A:Residues: 1-34, (0', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L',
A:Residues: 1-34, (0', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L',
A:Rote: this sequence has the Glm(17) and Glm(1) markers
R:Schmidt, W.E.; Jung, H.D.; Pallm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristalliserbaren monoklonalen Immunglol
A:Reference number: A91723; MUD:83289131; PMID:6884994
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
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F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A;Map position: 14g32.33-14g32.33
A;Introns: 99/1; 114/1; 224/1
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PMID: 4923144
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A;Reference number: S31866
A;Accession: S31866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, February 1993 A; Description: Screeing method for protein-protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: Homo sapiens (man)
C; Date: 06-Jan-1995 #sequen
C; Accession: S31866
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S31866
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A; Residues: 1-255 <FIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Keywords: immunoglobulin
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Best Local
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Best Local
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A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data A; Reference number: $72664
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-140, 'C', 142-374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-374 <KHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structure of abnormal heavy chains in human heavy-chain-deposition nce number: S69339; MUID:95262687; PMID:7744049
                                                                                                                                                                                                                                                                                                                Similarity
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                           ISKAKVQPREPQYYTLPPSRDELTKNQVŚLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                           EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                        EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                       ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                96.7%;
96.1%;
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                                                                                                                                                                                                                                                                                                                                                                      region;
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                                                                                                                                                                                                                                                                                                                Score 1219;
Pred. No. 1
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Ig gamma-1 chain C region - C; Species: synthetic synthetic

s (man) gene engineered and expressed
#sequence_revision 17-Mar-1997 #text_

#text_change 19-May-2000

protein-protein

interactions

of cloned

gene

A; Cross-references: EMBL: X70421; NID: g33068; PIDN: CAA49866.1; PID:g33069

F;23-255/Region: human Ig gamma-1 1-22/Region: Escherichia coli outer membrane chain C protein Þ precursor

Similarity Conservative 96.6%; Score 1217; DB 4; Pred. No. 1.1e-85; Length Indels 0; Gaps

0

NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT ESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 120 83 143

ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

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C; Accession: A23511
C; Accession: A23511
R; Huck, S.; Fort, P.; Crawford, D.H.; Lerrano, Nucleic Acids Res. 14, 1779-1789, 1986
A; Title: Sequence of a human immunoglobulin gar A; Reference number: A23511; MUID:86148507; PMT
A; Accession: A23511
A; Accession: A23511
A; Molecule type: DNA
A; Residues: 1-377 CHUC>
A: Cross-references: GB:X03604; GB:M12958; NID
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PT0207
PT0207
Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg,
Mol. Immunol. 28, 319-322, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Nucleotide sequence of chimpanzee A;Reference number: pT0207; MUID:91287716; A;Accession: pT0207
A;Molecule type: mRNA A;Residues: 1-234 cEHR> C;Superfamily: immunoglobulin C region; imm C;Keywords: immunoglobulin homology <1
                                                                                                                                                       A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 16
C;Superfamily: immunoglobulin C region; C;Keywords: immunoglobulin homology
F;20-85/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вp
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nes 215; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
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                         EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPKSCDTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
         EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
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                                                                                 Conservative
                                                                                                  90.3%;
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95.6%;
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                                                                                                                                                                                                                                                  OMIM:147120
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Pred. No. 2.8e-82;
                                                                               Pred. No. 2e-7
l; Mismatches
                                                                                                                  Score
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                                                                                                                    1138;
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PMID:2062315
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                                                                               Gaps
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       205
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                                                                                                                                                                                                                                                                                                                                                                                                   ဂ္ဂ
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 A;Note: the sequence of residues 42-76 was taken from the reference that follows R;Michaelsen, T.E.; Frangione, B; Franklin, E.C.

J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure.
                                                                                                                                                                                                           Ig gamma-3 heavy chain uiscur.
C;Species: Homo sapiens (man)
C;Date: 31-Dec:1979 #sequence_revision 23-Oct-1981 #text_change
C;Date: 31-Dec:1979 #sequence_revision 23-Oct-1981 #text_change
C;Accession: A90442; A92219; A90198; A93915; A02149
C;Accession: A90442; A92219; A90198; A93915; Franklin, E.C.
R;Frangione, A., A204-4308, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-377 <HUC>
C; Superfamily: immunoglobulin C
C; Keywords: immunoglobulin
F; 20-85/Domain: immunoglobulin
                                                                                                                                                                                                                                                                                                                                           RESULT 7
G3HUWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: A60764
C; Accession: A60764
R; Huck, S.; Lefranc, G.; Lefranc, 1989
                                                                                                                                                   Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion
A;Reference number: A90442; MUID:81021548; PMID:6774747
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, A;Teference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
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C; Date: 14-May-1993 #sequence_revision
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;20-85/Domain: immunoglobulin homology <IMM>
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Pred. No. 2
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2.8e-79;
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Gaps

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mutant:

gamma3

377

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with

an 1GHG4 16-Jul-1999

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Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Becies: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobul
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58
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A; Rosidues: 59-125, 'EB',128-226,228-289 <WOL>
A; Rosidues: 59-125, 'EB',128-226,228-289 <WOL>
A; Rote: this protein lacks most of the V region, all of the CH1 region, and part of the R; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.; Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deletion A; Reference number: A93915, WID:82247835; PMID:6808505
A; Contents: heavy chain disease protein Omm
A; Accession: A93915
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C:Superfamily: immunoglobulin C region; immunoglobulin
C:Keywords: duplication; glycoprotein; immunoglobulin;
F:203-270/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #st
F:6,140/Binding'site: carbohydrate (Asn) (covalent) #st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                idue segment (12 20)
A; Note: cysteines at positions 24, 27, 33, 33, 37, 42
R; Wolfenstein-Todel, C.; Frangione, B.; Prelli, F
R; Wolfenstein-Todel, C.; F
R; Wolfenstein-T
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A; Map position: 14q32.33-14q32.33
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Note: a carboxyl-terminal Lys is removed posttranslationally A; Note: a carboxyl-terminal Lys is removed posttranslationally A; Note: this sequence may represent an allelic form or another gamma chain subclass A; Note: this sequence may represent an allelic form or another gamma chain subclass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC.
A;Reference number: A90198; MUID:77021516; PMID:823945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A92219; MUID:77118561; PMID:402363
A;Contents: normal gamma-3 chains, sequence correspond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A90198
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Pred. No. 2e-78;
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          PIDN:CAB58438.1; PID:g6066056
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E.C.
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A; Residues: 238-275 <HOF>
R; Hofmann, T.; Parr, D.M.
submitted to the Atlas, M
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A;Accession: A90752
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                                                                                                                  NWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKT
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88.4%;
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J. Immunol. 125, 1048-1004, 2007
A; Title: The primary structure of a human 1
A; Reference number: A92809; MUID:81007873;
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A; Molecule type: protein
A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <
A; Note: Trp-156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. BioChem. 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chair
A; Reference number: A90752; MUID:80001357; PMID:113060
                                                                                                                                                                                                                                                                                                                F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,140-200,246-304/Disulfide bonds: #status experimental F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy cha
A;Reference number: A90253; MUID:72033500; P.
A;Contents: annotation; myeloma protein Sa,
C;Contents: annotation; myeloma protein Sa,
R;Frangione, B; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
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A; Map position: 14q32.33-14q32.33
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A; Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',1
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NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                       ERKCCVE----CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
                                                                                                                                          EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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PMID:118920
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3.8e-77;
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A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33·14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMI>
F;99-110/Region: hinge
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IGHRB
IGHRB chain C region - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984
C;Accession: A91749; A90290; A93928; A90245; A94416
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F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;142/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,141-201,247-305/Disulfide bonds: #status predicted F;27-83,141-201,247-305/Disulfide B;27-83,141-201,247-305/Disulfide B;27-83,141-201,247-305/Disulfide B;27-83,141-201,247-305/Disulfide B;27-83,141-201,247-305/Disulfide B;27-83,141-201,247-305/Disulfide B;27-83,141-201,247-305/Disulfide B;27-83,141-201,247-305/Disulfide B;27-83,141-201,247-305/Disulfide B;27-83,141-201,247-305/Disulfide B;27-83,141-201
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                                                                                                                                                                                                                                         LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
                                                                                                                                                                                                                                                                                                                                                       POVYTLPPSQEEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <PIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      determined from S.H.; De Vries,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.1%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e of a human immunoglobulin (
    MUID:83157104; PMID:6299662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1097; DB 1;
Pred. No. 2.2e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the germline ge
G.M.; Milstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Partial amino acid PMID:4192699
      A94416;
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#text_change
6; A02161
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in, C.
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                                    16-Jul-1999
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                                                                                           SISRSPGK
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A; Molecule type: protein
A; Rolecule type: protein
A; Residues: 132-143, 'E', 145-161 < FRUV
R; Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
R; Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
R; Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
R; Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
R; Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
R; Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
R; Hill, R.L.; Lebovitz, H.E.; Lebovitz, H.E.; Delaney, R.
R; Hill, R.L.; Lebovitz, H.E.; Lebovitz, H.E.
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A; Molecule type: mRNA
A; Kesidues: 88-103', M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A; Cross-references: GB.M16426; NID:g165111; PIDN:AAA31289.1; PID:g16:
A; Note: this sequence has the dl1 allotypic marker, 104-Met, and the R; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A; Title: Sequence studies of the Fd section of the heavy chain of rail A; Reference number: A90245; MUID:70110015; PMID:5461106
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A;Title: Sequence studies on the constant region of the A;Title: Sequence studies MUID:76135469; PMID:1243651
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Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy chain genes of rabbit 196; isolation of a
A;Reference number: A93928; MUID:83299917; PMID:6193512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;20-82/Domain: immunoglobulin homology <IM1>F;130-199/Domain: immunoglobulin homology <IM2>F;136-303/Domain: immunoglobulin homology <IM3>F;136-303/Domain: immunoglobulin homology <IM3>F;173/Binding site: carbohydrate (Asn) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 1-47, 'E', 49-71, 'PV', 72-128 < PRA>
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cs 18, 387-397, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVFIFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                                                                                                                                                                  TCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEY
                                                                                                                                                                                 KCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                                                                                                                                                                                                                                                                                             TCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLPITHQDWLRGKEF
EWEKNGKAEDNYKTTPAVLDSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQK
                                  KCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISV
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No. 4.
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Qy
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C:Superfamily: immunoglobulin C region; immunoglobulin
F;133-202/Domain: immunoglobulin homology <IMM>
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C;Superfamily: imn
F;133-202/Domain:
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 Qy
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A; Residues: 1-328 < KA
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R; Kacskovics, I.; St
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A; Residues: 1-328 <KAC>
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Best Local S
Matches 157
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                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                      Cross-references:
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                                                                                                            11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                             157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQYYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS
                                                                                             CPICPACE-SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT
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                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                      <KAC>
                                                                                                                                                                                                                                                                                   EMBL: U03779; NID: g433123; PIDN: AAA52217.1;
                                                                                                                                                                          68.9%;
70.1%;
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70.1%;
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                                                                                                                                                                        Score 868.5; DB 2
Pred. No. 5.9e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 868.5; DB 2
Pred. No. 5.9e-59;
2; Mismatches 32
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                                                                                                                                                           Mismatches
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21-Feb-1997
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 188
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                      A; Molecule type: protein
A; Residues: 4-68 <BIR>
R; Turner, K.J; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A; Title: Structure of heavy
                                                                                                                                 R; Birshtein, B.K.; Hussain, Biochemistry 10, 18-25, 1971
A; Title: Structure of heavy
                                                                                                        A; Reference number: A90352; A; Accession: A90352
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             A; Reference number:
                                                                                                       A; Accession:
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J. Immunol. 153, 3565-3573,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-277 <KA
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             A90359;
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Ig gamma-2 chain C region - guinea pig C;Species: Cavia porcellus (guinea pig) C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change C;Accession: A9453; A90352; A90359; A90384; A90385; A02151 R;Trischmann, T.M.
                                                                                                                                                                                                                                                                                                              submitted to the Atlas, April 1975 A; Reference number: A94553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: immunoglobulin C F;82-151/Domain: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THTCPPCP-APELLG-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKTKPPCPICPACEGPGPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQFSWYYD
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chain from strain 13 guinea MUID:71058486; PMID:5538616
                                                                                                                                                                                                                        Q.Z.; Cebra,
                                                                                                                                                         chain from strain 13 guinea MUID:71058471; PMID:5538606
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Pred. No. 8.9e-59;
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                    immunoglobulin-G(2).
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RESULT 15

147158
147158
1 gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
R;Racskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequence A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <ARC>
A;Cross-references: EMBL:003778; NID:9433121; PIDN:AAA52216.1; PID:9433122
C;Genetics:
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A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13.inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
Dain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin cregion; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C;Superfamily: immunoglobulin homology <IMI)
C;Superfamily: immunoglobulin homology <IMI)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;135-204/Domain: immunoglobulin homology <IM2>F;241-310/Domain: immunoglobulin homology <IM3>F;28-79/Disulfide bonds: #status experimental
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Biochemistry 10, 26-31, 1971
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R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from guinea A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
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A; Residues: 69-13; 312-329 < TUR>
R; Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
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                                            EPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDG
                                                                 EPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVG
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Copyright (c) 1993 - 2003 Compugen
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Biochemistry 20:2361-2370(1981).

-i- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE MARKERS.

-i- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.
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STRAND
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MEDLINE-81208100; PubMed-7236608;
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Biochemistry 9:3188~3196(1970).
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z J., Reichel W., Hilschmann N.;
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SEQUENCE (DISEASE PROTEIN WIS).
MEDITINE-81021548; PubMed-6774747;
Frangione B., Rosenwasser E., Prelli F., Franklin I
"Primary structure of human gamma 3 immunoglobulin
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
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theria; Primates; Catarrhini; Hominidae;
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MEDLINE-77118561; PubMed-402363;

Michaelsen T.E., Frangione B., Franklin E.C.;

"Primary structure of the 'hinge' region of human IgG3. Probable quadruplication of a 15-amino acid residue basic unit.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

INTERCHAIN DISULFIDE BY 12 DISULFIDE BONDS; IT HAS INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION NORMALLY PRESENT IN THE HINGE REGION.

PROTEIN WIS 1. MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS 1.
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SMART; SM00407; IGcl; 1.
PROSITE; PS00290; IG_MHC; 1
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Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence
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Wolfenstein-Todel C., Frangione
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InterPro; IPR003597; Ig_c1.
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MISCELLANEOUS: DISEASE PROTEIN ONM MAY REPRESENT AN ALLELIC FORM
OR ANOTHER GAMMA CHAIN SUBCLASS.

MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
IDENTICAL 15 RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
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MISCELLANEOUS: DISEASE PROTEIN
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[2]
MEDLINE=83001943; PubMed=6811139;
Takahashi N., Ueda S., Obata M.,
"Structure of human immunoglobuli
                     SEQUENCE OF 88-115
TISSUE=Fetal liver;
                                                          MEDLINE=82197621; PubMed=6804948; Ellison J.W., Hood L.E.; "Linkage and sequence homology of
                                                                        SEQUENCE OF 2-326 FROM MEDLINE=82197621; PubMe
                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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"A note of the amino acid sequence of mmunoglobulins gamma chains.";
"munoglobulins gamma chains.";
"A note of 16:923-925(1979).
InterPro; IPR003006; 1
InterPro; IPR003597; 1
InterPro; IPR003600; 1
Pfam; PF00047; ig; 3.
                                                    PIR; A02148; G2HU.
HSSP; P01857; 1FC1.
Genew; HGNC:5526; IGHG2.
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MEDLINE-69064124; PubMed-5782707;
Frangione B., Milstein C., Pink J.R.L.
"Structural studies of immunoglobulin
Nature 221:145-148(1969).
                                                                                                                                                                                                                                                                          Milstein C., Frangione B.; "Disulphide bridges of the heavy chain Biochem. J. 121:217-225(1971).
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denes.";
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"Comparison of the hinge-coding
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Cell 29:671-679(1982)
                                                                                                                                                                                                                                                                                                                                                         "Characterization of the immunoglobulins.";
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-121
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J. Biochem. 57:758-767(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.-C., Tung E., Fudenberg H.H.;
primary structure of a human IgG2 heavy
utlonary, and functional implications.";
                                                                                                                an email to license@isb-sib.ch).
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lotti V., Negri A.
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MEDLINE-83157104; PubMed=6299662;

Ellison J.W., Buxbaum J.N., Hood L.E.;

"Nucleotide sequence of a human immunoglobulin DNA 1:11-18(1981).
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                       MEDLINE-70207560; PubMed-4192699;
Pink JR.L., Buttery S.H., de Vries G.M.,
"Human immunoglobulin subclasses. Partial
constant region of a gamma 4 chain.";
                Biochem. J.
                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                      MEDLINE=84030930; PubMed=6313520; Bernstein K.E., Alexander C.B., M "Nucleotide sequence of a rabbit F-I haplotype.";
                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Ve.
Mammalia; Eutheria; Lagomorpha; Leporidae;
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buropean Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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MEDLINE=70110015; Pubmed=5461106;
Fruchter R.G., Jackson S.A., Mole L.

"Sequence studies of the Fd section
immunoglobulin G.";
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Hill R.L. Lebovitz H.E., Fellows R.E. Jr.,
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes."; Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
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Pratt D.M., Mole L.
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SEQUENCE OF 1-128.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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64.5%;
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Pred. No. 1.4e
34; Mismatches
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> A (IN E15 MARKER).
> E (IN REF. 2).
> VPV (IN REF. 3 AND 4.
> E (IN REF. 5).
> D (IN REF. 5).
> O (IN REF. 5).
TC--PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV
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les 38;
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GC2_C
                                                                                                                                                                                   SEQUENCE OF 227-31
MEDLINE=75036073;
Trischmann T.M., C
"Primary structure
                                                                          Oliveira
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"Structure of heavy chain from strain 13 guin immunoglobulin-G(2). II. Amino acid sequence and hinge region cyanogen bromide fragments." Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). 3. Amino acid sequence of thatfroystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-UUL-1986 (Rel. 01, Created 21-UUL-1986 (Rel. 01, Last see 21-UUL-1999 (Rel. 38, Last and 15-UUL-1999 (Rel. 38, Last and 19 gamma-2 chain C region. Cavia porcellus (Guinea pig).
                    Biochemistry 10:26-31(1971).
                                                                                         DISULFIDE BONDS.
MEDLINE-71058474;
                                                                                                                                                                       antibodies.";
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                                                         Oliveira B., Lamm M.E.
"Interchain disulfide
                                                                                                                                                                                                                                                                              Biochemistry 13:4796-4803(1974).
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=75036072;
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MEDLINE=71058486; PubMed=5538616;
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                                                                                                                                                  Biochemistry 13:4804-4811(1974).
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a J.J.;
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                                                                                             PubMed=4922544;
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InterPro; IPR003597;
InterPro; IPR003600;
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P20761;
                                                                                                                                                                                                    Gene 74:473-482(1988)
PIR; PS0018; PS0018.
HSSP; P01842; 7FAB.
                                                                                                                           InterPro; IPR003600; Pfam; PF00047; ig; 3
                                                                                                                                                                                                                                                       Brueggemann M.;
"Evolution of the rat
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=89232738;
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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15-JUL-1999 (Rel. 38,
Ig gamma-2B chain C re
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                                                                                       SM00410; IG_like; 1.
SM00407; IGcl; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00410; IG_like; 1.
SM00407; IGC1; 2.
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                                                                          PS00290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWFVDNKPVGNAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISKTKGAPRMPDVYTLPPSRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKN
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domain;
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                                                                          IG_MHC;
                                                                                                                                                                                                                                                                                               PubMed=3149946;
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                                                                                                                                           Ig_MHC.
Ig_c1.
Ig_like.
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67.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                     Immunoglobulin C
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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HTIW)
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                   (WITH
                                                     region
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.6e-63;
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                                                                                                                                                                                                                                                           heavy-chain
                                                                                                                                                                                                                                                                                                                                                                      Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                   A LIGHT CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                      Murinae;
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Best Local S
Matches 145
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GC3_MOUSE
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                                                                                                                                                                           between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There as a use by non-profit institutions as a modified and this statement is not removed. Usentities requires a license agreement (See http. or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                               EMBO
                                                                                                                                                                                                                                                                                                                                                                            P22436;

01-AUG-1991 (Rel. 19, Created)

01-AUG-1991 (Rel. 19, Last sequence updat

16-OCT-2001 (Rel. 40, Last annotation upd

Ig gamma-3 chain C region, secreted form.
                                                                        Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
                                                                                                                                                                                                                                                                        Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constar
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                    InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like
                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                               Transmembrane;
                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                       MEDLINE=85027161; PubMed=6092053;
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                      DOMAIN
                                                    Immunoglobulin domain; Immunoglobulin C region;
                                                                                                                                       HSSP;
                                                                                                                                                 B02156; G3MSC.
                                                                                                                                                                                                                                                               J. 3:2041-2046(1984).
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                                                                                                                                      P01857;
                                                                                                                                                           J00451;
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                                                                PS00290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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  98
114
                                         Alternative splicing.
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                                                                                                                                                           NOT_ANNOTATED_CDS.
                                                              IG_MHC; 1.
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Rodentia;
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Pred. No. 8.1e
34; Mismatches
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 HINGE.
                        CH1.
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55F8B64D48D460A6
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                                                                                                                                                                                                                                                                                                                                                                                                                                   329
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                                                                                                                                                                                                        ormatics and the EMBL outst
There are no restrictions
ong as its content is in
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HIIM)
HIIM)
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thi; Muridae; Murinae; Mus
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.1e-60;
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                                                    Glycoprotein;
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RESULT 9
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ID GC3M_M
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Best Local
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                                  InterPro; IPR003006; Tg_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_like.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3:
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
SEQUENCE
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restrained by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                "The
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-85027161; PubMed-6092053;
Mels J.A., Word C.J., Rimm D., Der-Balan
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 (EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 1
15-JUL-1999 (Rel. 1
Ig gamma-3 chain C
                                                                                                                       EMBL; J00451; AAB59655.1; -.
EMBL; V01526; CAA24767.1; ALT_SEQ.
PIR; A02155; G3MSM.
                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 328-398 FROM MEDLINE=84041483; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P03987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GC3M_MOUSE
                                                                                                                                                                                                                                                                      Nucleic Acids Res. 11:6775-6785(1983).
                                                                                                                                                                                                                                                                                                                       Komaromy
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                        PROSITE; PS00290; IG_MHC; 1.
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              Immunoglobulin
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                                                                                                              P01857;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGS : |||||:|| |::|| ||:|| ||:|| ||:|| ||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPGSSCPPGNILGGPSVF1FPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224
329 AA;
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                                                                                                                                                                                                                                                                                                                      Clayton
Alternative splicing.
              domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02, Creat
19, Last
38, Last
                                                                                                                                                                                                                                                                                                                    PubMed=6314258;
con L., Rogers J
                                                                                                                                                                                                                                                                                               the mouse immunoglobulin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 C
36228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region,
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64.7%;
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              Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 812.5;
Pred. No. 8.8e
85; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                       J.
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lon update)
e-bound form.
                                                                                                                                                                                                                                                                                                                       Robertson
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              G
                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                  constant
            region;
                                                                                                                                                                                                                                                                                                                                                                                                         G.P.,
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                                                                                                                                                                                                                                                                                             gamma
                                                                                                                                                                                                                                                                                                                       s:
                                                                                                                                                                                                                                                                                                                                                                                                          Martinez
            Glycoprotein;
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                                                                                                                                                                                                                      restrictions on
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murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).

PubMed=5073237;

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Best Local S
Matches 143
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=80045036; Pubm
Honjo T., Obata M., Ya
Takahashi N., Mano Y.;
                                                                                                                                                                                                                                                                                                   PO1868;
21-JUL-1986 (Rel. 01
21-JUL-1986 (Rel. 01
30-MAY-2000 (Rel. 30
19 gamma-1 chain C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
DOMAIN
CONFLICT
CONFLICT
CONFLICT
        SEQUENCE (MYELOMA MEDLINE=78242288; Adetugbo K.;
                                                                                                                                                                                        gamma
Cell 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
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                                                              SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MEDLINE=80012837; PubMed=113776; Rogers J., Clarke P., Salser W.; "Sequence analysis of cloned cDNA encoding par
                                                                                                             "Immunoglobulin gamma cloned in a bacterial Gene 9:87-97(1980).
                                                                                                                                                SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC MEDLINE=80202559; PubMed=6769752; Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataol
                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                   GC1_MOUSE
                                               Nucleic
                                                       "Sequence analysis heavy chain.";
                                                                                                                                                                                      "Cloning and complete nucleotide gamma 1 chain gene."; Cell 18:559-568(1979).
                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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 Evolution
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                                               Acids
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                                                                                                                                Seidman J.G., Peterlin
lobulin gamma 1 heavy cl
                                                                                                                                                                                                                                                                                                                                                                                                YFLYSKLTVDTDSWLQGEIFTCSVVHEALHNHHTQKNLSRSP
                                                                                                                                                                                                                                                                                                                                                                                                       PP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPGSSCPPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKE
of immunoglobulin subclasses.
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01, Last
39, Last
                   PROTEIN MOPC PubMed=98524;
                                                                                                                                                                                                                                     PubMed=115593;
                                              6:3305-3321(1979)
                                                                                                                                                                                                                                                                                                    region.
                                                                                                                                                                                                                            Yamawaki-Kataoka
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                                                                                                                       1 heavy
L plasmid.
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annotation update)
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HINGE.
CH2.
CH3.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
E -> G (IN REF. 2).
E -> G (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 801.5; DB 1
Pred. No. 8.9e-59;
5; Mismatches 41
                                                                                                                       chain gene:
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                                                                                                                                          Takahashi N., Kataoka T., Shimizu A., n B.M., Leder P., Honjo T.;
                                                                                                                                                                                                                                                                                                                                                   PRT;
                           21).
                                                                                                                                         в.м.,
                                                                                                                                                                                                         sequence
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Primary
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                                                                                                                               er P., Honjo T.;
structural gene sequences
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                                                                                            MOPC
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structure
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                                                                                            21)
                                                                                                                                                                     31C).
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                 327
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                                                               1mmunoglobulin
of.
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Best Local S
Matches 136
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                                                                                                                                                                                          DISULFID MOD_RES CONFLICT CONFLICT SEQUENCE
                                                                                                                                                                                                                                                 DISULFID
DISULFID
DISULFID
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CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:96446; Igh-4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
Pfam; PF00047; Ig; 3
SMART; SM00407; IGC1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01842; 7FAB.
GlycoSuiteDB; P01868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The disulphide bridges of a m Biochem. J. 126:837-850(1972).
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                                                                                                                                                                                                                                                                                                                                                      NON_TER
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Immunoglobulin dom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               veen the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                  180
                                     212
                                                        120
                                                                          152
                                                                                             60
                                                                                                               .99
                                                                                                                                  N
                                                                                                                                                              Similarity
                                               TISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                         PRDCG----CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQ
QPIMNTNGSYFYYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK
         PPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                    FNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEK
                                                                                                                          PKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
                                     TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNT
                                                                                                                                                                                                                                                                                                                                                               splicing
                                                                                                                                                                                          244
324
276
278
278
                                                                                                                                                     Conservative
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111
218
278
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102
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138
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                                                                                                                                                                                                                                                                                                                                                                        domain;
                                                                                                                                                                                                                                                                                                                                                                                  IG_MHC;
                                                                                                                                                                                                    302
324
276
278
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1.10
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1198
                                                                                                                                                                                           35704
                                                                                                                                                              62.7%;
                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                           MW.
                                                                                                                                                    47;
                                                                                                                                                    Score 789.5; DB 1
Pred. No. 6.7e-58;
7; Mismatches 41
                                                                                                                                                                                                                                                                  INTERCHAIN
INTERCHAIN
INTERCHAIN
                                                                                                                                                                                                  REMOVED POST-TRANSLATIONALLY
N -> D (IN REF. 3).
N -> D (IN REF. 3).
                                                                                                                                                                                                                                                                                                                  HINGE.
CH2...
CH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse
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                                                                                                                                                                                          -> D (IN REF. 3)
-> D (IN REF. 3)
A338812F3D1F2C93
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HIIW)
HIIW)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outstation
                  232
                                                                                                                                                     Gaps
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GC1_RAT

ID GC1_RAT

ID GC1_RAT

RC P20759;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1999 (Rel. 38, Last annotation update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 19 gamma-1 chain C region.

This norvegicus (Rat).

This norvegicus (Rat).
RESULT 12
GCLM_MOM
GCLM_MOM
AC P01869
DT 21-JUL
DT 01-AUG
DT 30-MAY
DE 19 gam
OS Mus mu
OC Eukary
OC Mammal
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Best Local S
Matches 137
                         GCIM_MOUSE STANDARD; PR P01869; P01869; P1-1986 (Rel. 01, Created) 01-AUG-1991 (Rel. 19, Last seque 30-MAY-2000 (Rel. 39, Last annot 19 gamma-1 chain C region, membr
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DOMAIN
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InterPro;
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                                                                                                                                                                                                                                                                                                                                     DISULFID
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                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brueggemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89232738; PubMed=3149946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Evolution of the rat
Gene 74:473-482(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS0017; PS0017.
                                                                                                                                                              213
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                                                                                                                                                                                                    153
                                                                                                                                                                                                                                                                              137;
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                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                       TPPTMDTDGSYFLYSKLNVKKEKWQQGNTFTCSVLHEGLHNHHTEKSLSHSPGK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00290; IG_MHC; 1.
                                                                                                                                     TPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                            HFSWFVDDVEVHTAQTRPPEEQFNSTFRSVSELPILHQDWLNGRTFRCKVTSAAFPSPIE
                                                                                                                                                                                                             KFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIE
                                                                                                                                                                                                                                                          PKSCDKTHTCPPCPAPELLGG----PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
                                                                                                                                                                                                                                        PRNCG--GDCKPC----ICTGSEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISQDDPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003006; Ig_MHC IPR003597; Ig_c1.
                                                                                                                                                                                                                                                                                                                  326
                                                                                                                                                                                                                                                                                                                            98
113
220
27
102
106
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111
140
246
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain;

    Last sequence update)
    Last annotation update)

                                                                                                                                                                                                                                                                                                                176
35946 MW;
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112
219
326
82
102
106
109
1111
200
Rodentia;
         Chordata;
                                                                                                                                                                                                                                                                                      62.3%;
58.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin C
                                                                                                                                                                                                                                                                              46;
                            membrane-bound
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INTERCHAIN
INTERCHAIN
INTERCHAIN
                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (P
; 013BAB45EF49B9DA CRC64;
                                                                                                                                                                                                                                                                                       Score 784.5; DB 1; Pred. No. 1.7e-57;
                                                                                                                                                                                                                                                                                                                                                                                                      HINGE.
CH2.
CH3.
Sciurognathi;
         Craniata;
                                                                           PRT;
                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma
                                                                           393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
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HTIW)
HTIW)
         Vertebrata;
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                            form.
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 Muridae;
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HEAVY
HEAVY
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Takahashi N., Mano Y.; "Cloning and complete gamma 1 chain gene."; Cell 18:559-568(1979).
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Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

-i- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
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domain.";
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Tyler B.M., Cowman A.F., Gerondakis S.D.
MRNA for surface immunoglobulin gamma
conserved transmembrane sequence and a
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Takahashi N., Mano
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MEDLINE=80045036; PubMed=115593;
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Cell 26:19-27(1981).
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PubMed=6799207;
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PIR; S00847; S00847.
HSSP; P01842; 7FAB.
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MEDLINE=88166903; PubMed=3127222;
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RT; SM00410; IG_like; 1.
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ART; SM00407; IG_MHC; 1.
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MEDLINE=73056887; PubMed=4565406;
de preval C., Fougereau M.;
"Determination of the primary str
                                                                              WYELOMA PROTEIN MOPC 173.

MEDLINE=74175517; PubMed-4831970;

BOUTGOIS A., FOUGETERM M., ROCCA-SETTA J.;

"Determination of the primary structure of a mouse IgG2a immunoglobulin; amino-acid sequence of the Fc fragment. In for the evolution of immunoglobulin structure and functif for the evolution of immunoglobulin structure and functifur. J. Biochem. 43:423-435(1974).
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"Structure of the constant and 3' untranslated
Balb/C gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=81076554; PubMed=6777755;
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                                                                                                                                                                                                                                                                                                                                         Nucleic
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Yamawaki-Kataoka Y., Miyata T., F
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ay C., Morchamps C., Rougeon F.;
mouse immunoglobulin gamma 2a and gamma
exons can be exchanged between genes in a
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Sciurognathi; Muridae;
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Matches 141
STRAIN=C57BL/6;
STRAIN=C57BL/6;
MEDLINE=82037861; PubMed=6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B.
"Multiple differences between the nucleic acid
"Multiple differences between the mouse.";
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 gamma-2A chain C region, B allele.
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SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
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Mammalia; Eutheria;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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and this statement is not removed.
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Rodentia;
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62.9%;
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Pred. No. 8
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Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).

-I- MISCELLABOUS: THE SEQUENCE DIFFERENCE STORY.
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SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
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              SVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                    CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
SDGSYFMYSKLRVQKSTWERGSLFACSVVHEVLHNHLTTKTISRSLGK
                                                       RGPVRAPQVYVLPPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLD
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60.1%;
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Pred. No. 1
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.9e-56;
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Title:
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein -
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DB
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1260
1 EPKSCDKTHTCPPCP
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1: sp_archea:*
2: sp_bacteria
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 EPKSCDKTHTCPPCPAPELL.....MHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                  sp_organelle:*
sp_phage:*
sp_plant:*
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sp_bacteria:*
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 471
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Q9FPQ8
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Q95M34
Q95M34
Q9R1A4
Q9R1A4
Q9D8L4
Q99L31
Q99L31
Q99L35
Q91Z05
Q9BSZ1
Q9BQB8
Q96BB9
Q9BU10
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        Q8tc77 homo sapien
Q95p98 homo sapien
Q8tc63 homo sapien
Q95m34 equus cabal
Q95m34 mus musculu
Q991c4 mus musculu
Q91c14 mus musculu
Q91c15 mus musculu
Q91c5 mus musculu
Q91c6 mus musculu
Q91c6 mus musculu
Q95cbb homo sapien
Q95bbb homo sapien
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 Q9bu10
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182.5	243.5	243.5	243.5	246	247	248	248	248.5	249.5	251	251	251	251.5	251.5	251.5	251.5	251.5	251.5	258	259	259	272.5	337	337	337	337	337	343
•	•	•	19.3	٠	•	•	•	•	•	•	•	19.9		20.0	•	•	•			•	•	•	•	26.7	26.7	26.7	26.7	27.2
259	484	481	479	497	416	500	496	480	479	496	494	384	489	488	484	482	481	481	426	487	486	684	618	614	613	613	588	613
13	11	11	11	4	4	4	4	11	1	4	4	4	11	11	11	11	11	11	11	11	11	13	4	4	4	4	4	11
Q90530	Q99LA6	Q8VCV5	Q99M22	Q8WY24	Q9NPP6	Q9BRV0	Q96DK0	Q91XE1	Q91WP5	Q96KX8	Q96K68	Q9UP60	Q8VCX4	Q91WR1	Q8VEA0	Q91x92	Q91WT1	Q91WT3	Q9DCD9	Q99KA4	Q91Z07	Q90544	Q96AA6	Q96GA6	Q8WUK1	Q96EY0	Q8WUX4	Q8VCX7
Q90530 ginglymosto	Q991a6 mus musculu	Q8vcv5 mus musculu	2 mus	Q8wy24 homo sapien	homo	homo	homo	1 mus		homo	homo	Q9up60 homo sapien	mus	. Q91wr1 mus musculu	mus	Q91x92 mus musculu	mus	Q91wt3 mus musculu	Q9dcd9 mus musculu	Q99ka4 mus musculu		4 ging		homo	Q8wuk1 homo sapien	homo	homo	Q8vcx7 mus musculu

ALIGNMENTS

Qy 121 ISKAKVQPREPQVYTLPPSRDE:	Qy 1 EPKSCDKTHTCPPCPAPELLGG Db 240 EPKSCDKTHTCPPCPAPELLGG Qy 61 NWYVDGVEVHNVKTKPREBQYN Db 300 NWYVDGVEVHNAKTKPREBQYN	QBTC77 ID QBTC77 AC QBTC77; AC QBTC77; AC QBTC77; AC QBTC77; DT 01-JUN-2002 (TrEMBLrel. 21, Created) DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DE Hypothetical 51.8 kDa protein. OC Mammalia: Eutheria: Craniata: Vertebrata: Eutelo OC Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo OX NCBL_TaxID=9606; RN [1] RP SEQUENCE FROM N.A. TISSUE-SPLEEN: RA TISSUE-SPLEEN: RA STRAUBERY R. Strausberg R.; RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. DR EMBL; BC024289; AAH24289.1; - RW Hypothetical protein. SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64; Query Match Best Local Similarity 97.0%; Pred. No. 4.8e-108; Matches 225; Conservative 3; Mismatches 4; Indels
ISKAKYQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180	EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60	OBTC77 PRELIMINARY; PRT; 471 AA. OBTC77; O1-JUN-2002 (TrEMBLrel. 21, Created) O1-JUN-2002 (TrEMBLrel. 21, Last sequence update) O1-JUN-2002 (TrEMBLrel. 21, Last sequence update) O1-JUN-2002 (TrEMBLrel. 21, Last sequence update) Hypothetical 51.8 kDa protein. Hypothetical 51.8 kDa protein. Hypothetical fire there is; Primates; Catarrhini; Hominidae; Homo. Hypothetical primates; Catarrhini; Hominidae; Homo. NCB1_TaxID=9606; [1] SEQUENCE FROM N.A. TISSUE-SPLEEN; Strausberg R; Strausberg R

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PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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Best Local
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PROSITE; PS00022; EGF_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS01187; EGF_CA; UNKNOWN_1.

PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

PROSITE; PS00240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
               Q8TC63;
Q8TC63;
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cells for immunotherapy in mouse models of prostatic cancer.";

Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).

EMBL; AF272774; AAK58686.1; -.

Interpro. Toponomica
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InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF-2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_CA.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Cr
01-DEC-2001 (TrEMBLrel. 19, La
01-MAR-2002 (TrEMBLrel. 20, La
Factor VII active site mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=21477448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
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n; PF00594; gla; 1.
n; PF00047; ig; 2.
n; PF00089; trypsin; 1.
RT; SM00181; EGF; 2.
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                                                                                                                                                                                                                                                 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                     ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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701 AA;
               (TrEMBLrel.
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                                        PRELIMINARY;
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97.0%;
                 21,
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Best Local
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                                   PROSITE;
NON_TER
SEQUENCE
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01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                              genes. III. Alignment of c-mu, c
Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
                                                            InterPro; IPR003006; Pfam; PF00047; ig; 2
                                                                                                                                                                                                    Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                Q95M34
                                                                                                                  Wagner B., Overesch G.,
Leibold W., Radbruch A.;
                                                                                                                                    MEDLINE-98383416; PubMed-9717671;
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                              Submitted
                                                                                                                                                                       Wagner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2002) to the EMBL; BC025985; AAH25985.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-JUN-2002 (TrEMBLrel. 21, La
Hypothetical 52.0 kDa protein.
                                                                                                         "Organization of the equine immunoglobulin
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=9796;
                                                                                                                                                                                                                                    (Fragment).
IGHC1.
                                                                                                                                                                                                                                                     Immunogobulin
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al Similarity
157; Conser
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1 (TrEMBLrel. 19, L
2 (TrEMBLrel. 21, L
lin gamma 1 heavy c
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473 AA; 5
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Conservative
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Primates;
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67.7%;
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90.5%;
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36;
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Pred. No. 7
        Pred.
                  Score 877.5;
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                                   A60BF2B01DEFD1F6
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Mismatches
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constant region
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                                    CRC64;
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               Length 337;
Indels
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databases

Indels Length

Gaps

59

290

350

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463; 9

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RESULT
Q99LC4
ID Q99LC4
AC Q8
AC Q8
DT 01
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Best Local
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                                                                                                                                                                Q99LC4;
Q99LC4;
01-JUN-2001
01-JUN-2001
01-JUN-2002
Similar to R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBR3V9:
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical SEQUENCE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2002) to the EMBL; BC024405; AAH24405.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                         RIKEN
                                                                                                                                                                (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence up
(TrEMBLrel. 21, Last annotation
RIKEN cDNA 1810060009 gene.
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                                                       Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                               PRT;
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                                                             Muridae;
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; Murinae; Mus
                                                       Euteleostomi;
Murinae; Mus
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003500; Ig_like.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003506; Ig_v.
Pfam; PF00047; Ig; 4

SMARR; SM00407; IGc1; 2.
SMARR; SM00400; IGc1; 2.
SMARR; SM00406; IGv; 1.
SMARR; SM00406; IGv; 1.
SMARR; SM00410; IG_MHC; UNKNO
SEQUENCE 463 AA; 51007 MW;
                                                                     Interruc;

Pfam; PF00047; 1g; 4.

SMART; SM00406; IGv; 1.

SMART; SM00410; IG_like; 2.

SMART; SM00290; IG_MHC; U
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                      Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misr "Cloning of cDNAs encoding for anti-white pine antibody (Mab 7, its light and heavy chains) a single chain antibody (scFV)."; submitted (MAY-1999) to the EMBL/GenBank/DDBJ EMBL; AF152372; AAD40243.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
Gammal heavy chain of Mab7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-2001)
EMBL; BC003435; AAHO:
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                                                                                                                                                                MGD; MGI:96446; Igh-4.
InterPro; IPR003600; Ig_Ike
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9R1A4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238
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137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEK 119
  437
437 F
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  AA;
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  48142
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                                                                                 UNKNOWN_1
  WW;
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Pred. No. 3.1e
#6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAA674C6BBC30783 CRC64;
  5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  K.M., Misra S.;
white pine blister rust monoclonal
chains) and construction of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1e-67;
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463 232

databases

Euteleostomi; Murinae;

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RESULT
Q9D8L4
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                                                                                                                                                                                                        RA Alzawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Alzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashtaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
              SMART; SM00409;
SMART; SM00407;
SMART; SM00406;
SMART; SM00410; 1
                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK007918; BABE2349.1; -.
HSSP; P01842; 7FAB.
MGD; MGI:96443; Igh-1.
                                                                                                                                                                                                   Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21085660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9D8L4
                                                                                      InterPro;
                                                                                                   InterPro;
                                                                                                               InterPro;
                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9D8L4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1810060009Rik protein.
1GH-1 OR 1810060009RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                               PF00047; ig; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
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                                                         918;

,42; 7FAB.

,96443; Igh-1.

o; IPR003599; Ig.

ro; IPR003597; Ig.c1.

IPR003600; Ig.like.

~~03006; Ig_MHC.

~~6; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
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Similarity 58.4%;
36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
            IG; 2.
IGc1; 3.
IGv; 1.
IG_like;
                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11217851;
  IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
  UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
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Pred. No. 6.9e-67;
7; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473
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; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus.
                                                                                                                                                                                                                                      K. -F.,
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Query Match
Best Local S
Matches 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             099L31;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00290; SEQUENCE 468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003596; Pfam; PF00047; 1g; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01842; 7FAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [nterPro;
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F SM00409,

AT; SM00407; IGC1; ...

ART; SM00406; IGV; 1.

ART; SM00410; IG_like; 1.

CM00410; IG_MHC; UNFOCOME SMOOTH 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tted (FEB-2001) to the EMBL/GenBank/DDBJ databases EC003878; AAH03878.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                           CPP--CPAPELLGGPSVFLFPPKJKDVLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
                             FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                               RAPQVYVLPPPBEEMTKKQVTLTCMVTDFMPEDIYVEMTNNGKTELNYKNTEPVLDSDGS
                                                                                                                          REPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGS
                                                                                                                                                                                                         VHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDGSYFMYSKLRVQKSTWERGSLFACSVVHEGLHNHLTTKTISRSLGK 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGPVRAPQVYVLPPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003597;
IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig_cl.
Ig_like.
Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                     61.3%; Score 772; DB 11; 62.9%; Pred. No. 5.4e-65; tive 31; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.
;; UNKNOWN_1.
;1 MW; 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 5.4c
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9DED57A514475FBB
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No. 6.1e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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; Murinae; Mus
  468
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RESULT
1091205
AC 05
AC 
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AC Q99L2
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DT 01-JU
DT 01-
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VQ
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Best Local S
Matches 141
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SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_MIC; UNKNO
SEQUENCE 473 AA; 52449 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003599; Ig. 1.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003600; Ig_11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfan; PF00047; 1g; 3.
                                                                                                                                                                                                                                                                                                                           O91Z05; PRELIMINARY;
O91Z05;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
Hypothetical 51.9 kDa pro
AU044919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q99L25 PRELIMINARY; rx1, Q99L25; Q99L25; Q1-JUN-2001 (TrEMBLrel. 17, Created) Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update) Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                   AUD044919.
AUD44919.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (FEB-2001)
Strausberg R.;
Submitted (JUL-2001) to the
EMBL; BC010327; AAH10327.1;
MGD; MGI:2144967; AU044919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC003888; AAI
HSSP; P01842; 7FAB
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                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGS
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62.9%;
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19,
21,
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MW; BE9889B7986DA155
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                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation updat
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Pred. No. 5.5e
31; Mismatches
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                                                                     EMBL/GenBank/DDBJ
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Sciurognathi;
                                                                                                                                                                                                                           Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473
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thi; Muridae;
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5.5e-65;
                                                                                                                                                                                                                                                               Vertebrata;
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                                                                                                                                                                                                                                 Muridae;
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; Murinae; Mus
                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                 Murinae;
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                                                                                                                                                                                                                                 Mus
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RESULT
Q8R3H6
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                    RESULT 13
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Best Local S
Matches 140
                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                         QBR3H6;
Q1-JUN-2002 (TrEMBLrel. 21, Creat O1-JUN-2002 (TrEMBLrel. 21, Last O1-JUN-2002 (TrEMBLrel. 21, Last Hypothetical 51.7 kDa protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; 19; 3.

PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

Hypothetical protein.

SEQUENCE 473 AA; 51946 MW; CF625F0089:
                                                                                                                                                                                                                                                                  Submitted (MAR-2002) to the EMBL; BC025447; AAH25447.1; Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                             Q8R3H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000345; CytC_heme_bind
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                 Strausberg
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               12
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                                                                                           356
                                                                                                              114
                                                                                                                                    296
                                                                                                                                                                            236
                                                                                                                                                                                                                    140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54
                                                                                                                                                      54
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                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPKSCDKT-HTCPP-----CPAPELLGGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSH
                                                                                                                                                                                     EPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                         DDPDVQISWFVNNVEVHTAQTQTHREDXNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDL
                                                                                                                                             EDPEVKENWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSE
                                                  ENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
                                                             NNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                           EPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSE
                                                                                                                                                                                                                                                          al protein.
474 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                           51748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.7%;
                                                                                                                                                                                                                            59.7%;
58.6%;
                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                                                                                   Last sequence up
                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 752.5; DB 1
Pred. No. 3.9e-63;
                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF625F008932AF12
                                                                                                                                                                                                                                                          8608B57C6CD2874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                   ed. No. 3.9
                                                                                                                                                                                                                                       752.5;
                                                                                                                                                                                                                                                                                                                                                                                                                             474
                                                                                                                                                                                                                              3.9e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                             ₽
                                                                                                                                                                                                                                                                                                                                                                                  on update)
                                                                                                                                                                                                                                       DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56;
                                                                                                                                                                                                                   56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                        databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473
                                                   474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354
                                                                                           415
                                                                                                              173
                                                                                                                                    355
                                                                                                                                                      113
                                                                                                                                                                                               53
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Q9BSZ1

PRELIMINARY;

PRT;

375

B

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RESULT 14
Q9BQBB
ID Q9BQB
ID Q9BQB
AC Q9BQB
DT 01-U0
DT 01-DE
DE UNKO
OC EUKAI
OC MANNHA
OC NCBI
RN [1]
RN [1]
RN [1]
RN [2]
RN [2]
RN SEQUE
RC TISSU
RA SUDMi
RL SUDMi
RL SUDMi
RL SUDMi
RL SUDMi
RN [2]
RN [2]
RN [1]
RN 
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BSZ1:
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
Hypothetical 41.3 kDa protein
                       Submitted (JAN-2001) to the EMBL; BC006180; AAH06180.1; EMBL; BC001872; AAH01872.1; H$SP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat update)
Unknown (protein for MGC:1905) (protein for MGC:1
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein SEQUENCE 375 AA; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                              Strausberg R.;
                                                                                                                                   TISSUE-LYMPH;
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                            Strausberg
                                                                                                                                                                                                                                                  TISSUE=MUSCLE;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BQB8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         о во в
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
    [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interPro; IPR003597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC004476; A/
P01857; 1FC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SVGSFFLYSKLTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAK-VQPREPQVYTLPPSRDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESHPNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVS
                                                                                                                                                                                                       (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH04476.1;
                                                                                                                                                                                                                                                                                                                                             Primates;
                                                                                                                                                                                                                                                                                                                                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig_cl.
Ig_like.
Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Ιg
                                                                                                                                                                                                       ξ
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33.6%;
                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 347; DB 4; 1
Pred. No. 9.8e-25;
8; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                    Catarrhini;
                                                                                                                                                                                                                                                                                                                                                              Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B1A0A0998F473619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           597
                                                                                                                                                                                                                                                                                                                                                                Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ą
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                                                                                                                                                                                                                                                                                                                                           Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                          update)
MGC:1228).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232
                                                                                         databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143
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Q96BB9
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Best Loc
Matches
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Best Local S
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Q96BB9;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ
EMBL; BC015760; AAH15760.1; -.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein SEQUENCE 597 AA; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 4.
SMART; SM00406; IGv; 1.
SMART; SM00406; IG_like; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SEQUENCE 597 AA; 65300 MW; 2DAFA
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=B-CELL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical 65.0 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003600;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003597;
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                                                                                                                                                                                                                                                                       Local Similarity les 72; Conserv
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                                                                                       426
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72; Conserv
NLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVS
                                                                                       YRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAK-VQPREPQVYTLPPSRDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNST
                                          T-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SVGSFFLYSKLTVD
                                                                                                                                                                                VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESHPNAT
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(TremBLrel. 19, Last seq
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Pred. No. 1.8e
48; Mismatches
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Pred. No. 1.8e-24
8; Mismatches 8
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Post-processing: Minimum Match 0%
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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                                                   Human IgG1 hinge/F
Human IgGgammal hi
Human partial IgG1
Human IgGgammal hi
Human immunoglobul
Human IgG Fc fragm
Human immunoglobul
                                                                                                                                                                                                                       Description
Protein from pCd51
Fusion protein of
Human immunoglobul
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1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225
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AAY30201	AAU81014	AAE12715	AAW49816	AAR43339	AAM49203	AAB28694	AAY31669	AAW05829	AAY24153	AAW10550	AAB28692	AAW10552	AAR26530		AAW14765	AAW14764	AAB28693		AAY15123	AAW18575	AAW18574	ABB07681	AAW4 9073	AAW83962	\sim	AAP93558	o	AAR43685	\vdash	78	57	AAE21960	9	AAB04071
cha ir	B7-related protein	Human recombinant	Amino acid sequenc	Completely humanis	∍.	Н	Human IgGl chain C	Humanised 1D10 ant	e LOX-1 ext	<pre>IgG1 polypeptide.</pre>	Fc-huAGP-1 (95-281	acid		Fc-muAGP-1 (120-29	solub	ble	GP-1	Mouse MK61-human I		artif	nase artif				c pept	human I	nce of		TR-Fc-delt			deat	IgG gamma	Zcytor 10::IqG qam

ALIGNMENTS

RESULT 1

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Recombinant protein expression system for fusion protein production		N-PSDB; AAT80158.	WPI; 1997-402624/37.		Sgarlato GD;		(TECH-) TECHNOLOGENE INC.		31 - TAN - 1006 : 06110 - 05050/3		31-JAN-1997; 97WO-US01470.		07-AUG-1997.		W09728272-A1.		Homo sapiens.		carboxypeptidase; IgGl; immunoglobulin; hinge region; Fc.	Fusion protein; hydrophilic spacer; recombinant; expression system;		Human IgG1 hinge/Fc region.		16-MAR-1998 (first entry)		AAW26232;		AAW26232 standard; Protein; 232 AA.	AAW26232

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                                                                                                                                                                                                                                                                  Human; AGP-1; type II transmembrane protein; cytostatic; antiviral; antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV human immunodeficiency virus; apoptosis; proliferative disorder; cancer; hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cterminus, of a first domain comprising a protein of interest, a second domain comprising a hydrophilic spacer and an affinity domain, each domain comprising amino acid residues. The present sequence represents the hinge/Fc region of human IgGl, used in example 3 of the present invention. The recombinant vector is used for the production of authentic recombinant proteins of interest. The method of the invention is useful for the expression of fusion proteins capable of isolation by affinity chromatography in pro- or eukaryotic cells. This method allows for the efficient cleavage and generation of authentic proteins of interest that do not contain extraneous (i.e. non-naturally occurring)
 WPI; 2000-665240/64
                                Hsu H,
                                                                                             16-APR-1999;
                                                                                                                           24-MAR-2000;
                                                                                                                                                                                                                                                    arteriosclerosis; IgGgammal
                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-2001
                                                                                                                                                          26-OCT-2000
                                                                                                                                                                                                                                                                                                                                                              Human IgGgammal hinge, CH2 and CH3 regions
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                             Meng S;
                                                              AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recombinant vector has been developed which comprises a ide sequence encoding a fusion protein. The fusion protein es three domains joined together in order, from N-terminus to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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                                                                                                                           2000WO-US08004
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                              INC
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97.08;
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Pred. No. 2.1e-90;
3; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                    osteolytic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins have increased that the action of the AGP-1 containing fusion proteins have increased that the AGP-1 containing fusion proteins have increased the AGP-1 containing fusion proteins have increased that the AGP-1 containing fusion proteins have increased the AGP-1 containing fusion proteins have increased that the AGP-1 containing fusion proteins have increased the AGP-1 containing fusion proteins have a contained the AGP-1 containing fusion proteins h
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                                                                                                                                                                                                                                                                                                                                                                          therapy; bone long hypercalcaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY72915 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      may also be treated.
biological activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  partial IgG1 protein
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225; Conserv
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                                                                                                                                                                                                                                                                                                                                                                        orotein; osteoprotegerin;
oss; osteoporosis; Paget
osteopenia; osteonecros;
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97.0%;
                                                                                                                                                                                                                                                                                                                                                  prosthetic loosening;
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                                                                                                                                                                                                                                                                                                                                                                        rosis; Paget's disease; ost osteonecrosis; rheumatoid
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Pred. No. 2.1e-90;
3; Mismatches 4
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Matches 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3;
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                                                                                                                                                                                                                                                                                                                                                                                               lytic bone disease; multiple myeloma; immunoglobulin; osteosclerotic bone metastasis; OPG; osteoprotegrin; osteoclast formation inhibition; bone resorption inhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; IgGgamma1; anticancer; Antimetastatic; Osteogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human IgGgammal hinge, CH2 and CH3 regions
                                                        (AMGE-) AMGEN
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97.0%;
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Pred. No. 2.1e-90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for the prevention or treatment of lylic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegrin) polypeptide or OPG fusion protein. The OPG proteins (see AAB808905) can inhibit formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The present sequence can be used to generate fusion proteins of OPG and immunoglobulin, for use in the present invention. The generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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                                                                                                                                                21-APR-2000; 2000US-0559001
                                                                                                                                                                                                                                                  01-NOV-2001
                                                                                                                                                                                                                                                                                                WO200181405-A2
                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE15347 standard; Protein; 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion proteins can exhibit increased circulating half-lives and
                                                                                                                                                                                                 19-APR-2001;
                                                                                               (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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peptide -
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                                                JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                                                                                                                                                                                                                                                                                                                                                                                                                      erythropoietin;
                                                                                                                                                                                                                                                                                                                                                                                               myelosuppressive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           times, thereby providing a more sustained activity.
                                                   Elliott SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                 2001WO-US12836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.2%;
97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         Epo; haematocrit; anaemia; kidney function; IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IgG) gamma 1 constant heavy chain hinge region
                                                   Browne
                                                                                                                                                                                                                                                                                                                                                                                               therapy; anti-viral drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1225
Pred. No.
                                                   JK,
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                                                   Sitney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              particularly associated an osteoprotegrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
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           04-JUL-2001; 2001WO-JP05788
                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                             01-JUL-2002
                                                                                                          Misc-difference
                                                                                                                                    Misc-difference
                                                                                                                                                                                                      Protein A; immunoglobin G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising administering less frequently and at 10
                                                                  WO200204602-A1
                                                                                                                                                                              Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              easing and maintaining hematocrit in mammal suffering from anemia, rising administering hyperglycosylated analog of erythropoletin frequently and at lower molar amount of recombinant human bropoletin -
                                                                                                                                                                            sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                            ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                         /note=
169
                                                                                                                                   Location/Qualifiers 168
                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.2%;
97.0%;
                                                                                                                                                                                                                                   amino
                                                                                                                    "encoded by GAC"
                                                                                          "encoded by ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                      IgG; antibody; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   method for increasing
                                                                                                                                                                                                                                                                                                                  233
                                                                                                                                                                                                                                  acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1225; DB 23;
Pred. No. 2.1e-90;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and maintaining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
                                                      immunosuppressive; dermatological; antiinflammatory; antidiabetic; neuroprotective; antirheumatic; antiarthritic; antiasthmatic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia grav: multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphor glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephrit pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a transformant yeast that can present protein A or its fragment on its cell surface. The yeast can be used for detecting or isolating the Fc part of immunoglobulin (1g)G. The yeast is useful for a stable supply of highly active catalytic antibody e.g. by screening novel functional molecules and in isolating Fc-carrying secretory proteins. The yeast of the invention is capable of adhering specifically to a combinatorial antibody library with an Fc-carrying antibody component. The current sequence represents the human IgG Fc fragment
                                            graft-versus
                                                                                                                                                                                                                                   Human immunoglobulin gammal constant region protein SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A or
                                                                                                                                                                                                                                                                                                      ABB81490
                                                                                                                                                                                                                                                                                                                                      ABB81490 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanaka A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-2000; 2000JP-0206689
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                                                                                                                                                                                                         Ztnfr12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                  PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment, particularly with the ZZ domain, on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                            host disease;
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                                                                                                                                                                                                       tumour necrosis factor receptor; cytostatic;
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                                                                                                                                                                                                                                                                                                                                    Protein;
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97.0%;
                                           graft rejection; Crohn's
                                                                                                                                                                                                                                                                                                                                      251
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Pred. No. 2
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                                                                                                        lymphoma;
                                                                                                                                        gravis;
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s useful for
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                                                                                                                                                                                                                                                                                                                                                          DЪ
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                                                                                                                                                                                                                                                                                                                                                                                                  designated zinfr12 (1) (1) has cytostatic, immunosuppressive, CC dermatological, antiinflammatory, neuroprotective, antidiabetic, CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive activities, and can be used in gene therapy. (1) can be used for CC (e.g. ZTNF4), for treating disorders and diseases associated with B CC (e.g. ZTNF4), for treating disorders and diseases associated with B CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for CC inhibiting the proliferation of tumour cells. (1) is useful for treating CC autoimmune disorders such as systemic lupus erythematosus, mysthenia CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, crematoid arthritis, bronchitis, emphysema and end stage renal failure correnal disease such as glomerulonephritis, vasculitis, chronic lymphoid CC leukaemia, nephritis, and pyelonephritis, and for treating renal CC meoplasms, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft-versus host CC disease, graft rejection and Crohn's disease. (1) is useful for CC modulating the immune system, for regulating B cell responses and CC development, for modulating development of other cells, antibody CC production and cytokine production, and for modulating T and B cell communication. Human Ztnfr12 is located to chromosome 22q13.2. The present sequence represents homan immunosolobulin gammal constant region, which is useful for a promote from the present invention.
                         Qy
                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                     Matches 225;
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20-DEC-2000;
28-JUN-2001;
29-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 143; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2tnfr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-2001; 2001WO-US47018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes
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DB; ABN89435.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolated human tumor necrosis factor receptor polypeptide, termed 12, useful for treating autoimmune disorders, emphysema, end renal failure or renal disease and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JA,
                                                                                                                                          80
                                                                                                                                                                           61
                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                 1
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                            NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                               EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMTSRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                           used
                PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                      ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                          NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                     ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Хu
                                                                                                                                                                                                                                                                                                                                                           251
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2000US-257131P.
2001US-301715P.
2001US-315565P.
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                           in an example from the present invention.
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                                                                                                                                                                                                                                                                                                    97.2%;
97.0%;
                                                                                                                                                                                                                                                                                  Score 1225; D
Pred. No. 2.3e
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a human tumour necrosis factor
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                                                                                                                                                                                                                                                              DB _
2.3e-90;
`s 4;
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                                                                                                                                                                                                                                                                                    0;
251
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                                                                                                                                                                                                                                                                                  Gaps
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Query Match
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Matches 225
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19-DEC-1997;
09-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a fusion peptide which consists of the extracellular domain of a mammalian oxidized LDL (low density lipoprotein) receptor, fused to a partial heavy chain of a mammalian immunoglobulin containing all or part of the constant region. Oxidize LDL is a denatured form of LDL occurring in patients having arteriosclerosis or hyperlipidaemia, and the fusion peptide can be used for the assay of oxidized LDL in biological samples from such patients, for the diagnosis of the disorders. It can also be used therapeutically for the prevention and treatment of arteriosclerosis hyperlipidaemia. The present sequence represents the protein from the vector DNA of pcd3inegl comprising human IgGI Fc region genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 92-96; 105pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusion peptide for assay of oxidized LDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kakutani M, Masaki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9932520-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY24154 standard; Protein;
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hes 225;
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density lipoprotein; receptor; detection; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                    ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                  NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                     EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                        PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                            NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 AA;
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pCd51neg1 comprising human IgG1 Fc
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97JP-0364981.
98JP-0349648.
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97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                Score 1225; DB 20;
Pred. No. 2.4e-90;
3; Mismatches 4;
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RESULT 9 AAB47590

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                                                                                                                                                                                                                                                                                                              This sequence represents a fusion protein which comprises the mouse heat shock antigen (HSA) fused to human IgG1 Fc. This protein may be used in the method of the invention for inhibiting destruction of tissue initiated by autoreactive T cells (GATC). The method is especially used to treat subjects suspected of having autoimmune diseases, particularly multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, psoriasis, diabetes and allergy, also transplant rejection. Transgenic mice that express human CD24 on their T cells are useful as models for testing drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting tissue destruction by autoreactive T cells, useful treating autoimmune diseases, by administering a heat-shock antigen/CD24 polypeptide or its antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; psoriasis; diabetes; allergy;
                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
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DB; AAH43523, AAH43524.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heat shock
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                      against autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNIV OHIO
                                   NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                               ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                            EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                   NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF, 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                   ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rejection;
                                                                                                                                                                                                                                                                                287 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 10; 34pp; English
                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                          97.2%;
97.0%;
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                                                                                                                                                                                                                                Score 1225; DB 22
Pred. No. 2.8e-90;
3; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rat; signal transducer;
re T cell; aTC;
                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                              Indels
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RESULT 11
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 Zcytor 10::IgG
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                      11-APR-2001
                                                                 AAB04071
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 13-15; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant alkaline phosphatase (AP)-antibody fusion protein -comprises AP fused downstream of antibody heavy or light chain, useful as immunoassay reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR91806 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TOYJ ) TOSOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP08070875-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunoglobulin gamma heavy chain constant region sequences.
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DB; AAT27385.
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                                                                                                                                                                  218
                                                                                                                                                                                       121
                                                                                                                                                                                                                     61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                             Similarity
                                                                 standard;
                                                                                                                                   PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                      NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                      PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                  ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                           ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hinge;
                                                                                                                                                                                                                                                                                                                                             329
                                                                                                                                                                                                                                                                                                  Conservative
                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORP
gamma
                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94JP-0211035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94JP-0211035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion protein; chimera; if
                                                                 Protein;
                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                            97.2%;
97.0%;
 fusion
peptide.
                                                                 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329
                                                                                                                                                                                                                                                                                                Score 1225; DB 17
Pred. No. 3.2e-90;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                 A
                                                                                                                                                                                                                                                                                                                      DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ımmunoassay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H-chain;
                                                                                                                                                                                                                                                                                                  4 ;
                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-region;
                                                                                                                                                                                                                                                                                                                       329;
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                      use in
                                                                                                                       329
                                                                                                                                           232
                                                                                                                                                                                                                                                                                                                                                                                                            of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CH1;
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                       157
                                                                                                                                                                                                           217
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В
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                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                      considered the presence of a test ligand and comparing levels of activity of mouse zcytor10 protein by culturing the cells in the presence of a test ligand and comparing levels of activity of mouse zcytor10 cc in the presence and absence of the test sample. Similarly, detection of zcytor10 receptor ligand within a test sample can be achieved. Cc for method comprising contacting a test sample containing an amino cc acid sequence from Cysls or Gly25 to pro230 of the zcytor 10 cc cytokine receptor and detecting the binding of the polypeptide to a cligand in the sample. Specified peptide fragments of the zcytor 10 cc ytokine receptor and the methods described are used to identify cligands that stimulate the proliferation and/or development of the cytokine receptor and myeloid cells. Peptide fragments of the cytokine receptor are useful for treating lymphoid, immune, inflammatory, splenic, blood or bone disorders and for generating cc secreted human zcytor 10 heterodimer is constructed. In this construct the extracellular cytokine binding domain of zcytor 10 cc is fused to the heavy chain of IgG gamma and the extracellular cytokine receptor subunit (an interlakin receptor subunit is fused to human kenna light
                                                                                                                                                                                                                 Query Match
Best Local S
Matches 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand; binding; detection; modulation; recombinant cell; haematopolatic cell; lymph; haematopolatic cell; lymph; immune system; blood; bone; inflammatory response; inflammation;
                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 17; Page 120-121; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lymphoid and myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cytokine receptor mouse zcytor 10, useful for detecting ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200068381-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spleen;
                                                                                                                                                                                                                                                                                                        interleukin receptor subunit) is fused to human kappa light chain (See GENESEQ record AAA54474). The two sequences are fused cogether using two primers (AAA54475, AAA54476).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stimulate proliferation or development of haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-016096/02
                                   121
                                                                     159
                                                                                                      61
                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          numan.
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g a nucleotide which encodes the zcytor 10 cytokine enables the production of recombinant cells expressing the
                                                                                                                                                              EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                        NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                           EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
ISKAKGQPREPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                   ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                     NWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                         330
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-US12924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Foster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0309861.
                                                                                                                                                                                                                                97.2%;
97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hammond
                                                                                                                                                                                                                                Score 1225;
Pred. No. 3.
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ŀok
                                                                                                                                                                                                                                .3e-90;
                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                 0;
                                                                                                                                                                                                               Gaps
                                  180
                                                                    218
                                                                                                       120
                                                                                                                                           158
 278
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RESULT 12
ABB81641
Дb
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                                                                                antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic activities, and can be used in vaccines. (I) or an antibody binding (I) can be used for suppressing the immune system for reducing rejection of tissue or organ transplants and grafts and for treating T-cell specific leukaemias or lymphomas and autoimmune diseases including rheumatoid arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel disease and Crohn's disease. The antibodies can also be used for treatin immunologic renal diseases, glomerulonephritis, mesangioproliferative disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or vasculitis associated with lupus, polyarteritis, scleroderma, HIV-relate diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the antibodies can also be used for renal or urological neoplasms and multiple myelomas, asthma, bronchitis, emphysema and other chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis; mesangioproliferative disease; chronic lymphocytic leukaemia; bronchitis; secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma; haemolytic uraemic syndrome; renal neoplasm; urological neoplasm; emphysema; chronic airway disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; immune system, T-cell specific leukaemia; lymphoma; lupus; autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV; diabetes mellitus; inflammatory bowel disease; Crohn's disease; ast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antidiabetic; nephrotropic;
                                                                                                                                                                                                                                                                                                                                       and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic, antiheumatic, antiarthritic, neuroprotective, antiinflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 7; Page 171-172; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel zcytor19 polypeptides and polynucleotides useful for stimulating immune responses in animals for producing antibodies, and for treating autoimmune diseases, leukemia and asthma - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-2000;
07-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200244209-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB81641 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABQ73076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZYMO ) ZYMOGENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-2001; 2001WO-US44808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                             present invention describes an isolated human zcytor19 protein (I),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-527700/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  zcytor19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma 1 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-253561P
2001US-267211P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytokine receptor; immunosuppressive; cytostatic; ntiarthritic; neuroprotective; antiinflammatory; phrotropic; dermatological; anti-HIV; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novak JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crohn's disease; asthma;
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airway diseases. Human zcytor19 is located to chromosome 1, more specifically to chromosome 1p36.11. The present sequence represents a human IgG gamma 1 heavy chain protein, which is used in an exampl

for treating

HIV-related

present invention

SO

Sequence

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RESULT 13
AAE21960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
composition comprising a death domain containing receptor (DR6) agonist or antagonist. The method is useful for treating or preventing a T cell mediated condition or a Th2 cell mediated condition in a mammal. A DR6
                                          The invention relates to a method for treating or preventing a mediated condition or a Th2 cell mediated condition in a mamma method comprising administering to the mammal a pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                              H. pylori-associated ulceration; antinflammatory; vasotropic; virucide; acquired immunedeficiency syndrome; AIDS; human immunodeficiency virus; HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective; adult respiratory distress syndrome; ARDS; cyrostatic; thyromimetic;
                                                                                                            Disclosure;
                                                                                                                                                    composition comprising
                                                                                                                                                                                    Treating or
                                                                                                                                                                                                                                                                                                                                     30-APR-2001; 2001WO-US11735
                                                                                                                                                                                                                                                                                                                                                                   15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                 WO200185209-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis; transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis; autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; therapy; death domain containing receptor; DR6; receptor; anaemia; apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;
                                                                                                                                                                                                                                                                             (ELIL ) LILLY & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                           dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE21960 standard; Protein; 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                               JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279
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                                                                                                                                                                      or multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    μ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
                                                                                                       Page 132-133; 133pp; English.
                                                                                                                                                               preventing T cell or Th2 cell mediated condition e ultiple sclerosis in mammal, comprises administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain containing receptor (DR6).protein-related protein.
                                                                                                                                                                                                                                                                                                        2000US-203015P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatotropic;
                                                                                                                                                                                                                                                                             ELI.
                                                                                                                                                                                                                                               Na
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97.0%;
                                                                                                                                                      death
                                                                                                                                                                                                                                            Song
                                                                                                                                                    domain containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1225; DB 23
Pred. No. 3.3e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibacterial.
                                                                                                                                                                                                                                               YYH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                            Yang
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                                                           mammal.
                                                                                                                                                   DR6 agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 14
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Best Local
                                                                                                                                                                           muscular; lymphoid; immune; inflammatory; spleenic; blood; bone; infection; immunosuppression; cytoftoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.
                                                                                                                                                                                                                                                                             Zcytor17; chromosome 5; 5q11; cytokine receptor;
                                                                                                                                                                                                                                                              antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS) or a condition or symptom related to the above mentioned diseases in a mammal. An DR6 antagonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with immunodeficiency, aberrant apoptosis, bacterial, viral or microbial infection, complications of infection, banan immunodeficiency virus (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pyloriassociated ulceration
                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB05736 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               associated ulceration, cytoprotection during cancer treatment, recuperation from chemotherapy, recuperation from irradiation therapy, or a condition or symptom related to the above mentioned diseases in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with aberrant apoptosis, graft-versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma, atopy, inflammatory bowel disease, vasculitis, psoriasis, pancreatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hashimoto'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lashimoto's thyroiditis, Graves disease, transplant rejection, systemic upus erythematosus, autoimmune dermatosis, autoimmune cardiopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin-dependent diabetes mellitus, cancer, multiple sclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                                                                                                                              antiviral; antirheumatic; antiarthritic;
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97.0%;
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Pred. No. 3
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                                                                                                                                                                                                                                                              cytostatic;
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26-JUN-2001; 2001WO-US20484.

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Czytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, 
cantirheumatic, antiarthritic and muscular activities. The zcytor17 
cz antirheumatic, antiarthritic and muscular activities. The zcytor17 
cz proteins are useful for treating and diagnosing lymphoid, immune, 
cz inflammatory, spleenic, blood or bone disorders. Agonists or 
canti-zcytor17 antibodies are useful in stimulating cell-mediated 
cz inmunity and for stimulating lymphocyte proliferation, such as in the 
cz treatment of infections involving immunosuppression, including certain 
cz vital infections. They are also useful for inducting cytotoxicity and 
cz treating leukopenias. Antagonist of zcytor17 polypeptides are useful 
cz for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple 
cz clerosis), inflammatory diseases (e.g. Czohn's disease), cancer, 
cz chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to 
Canaba93843 and ABB05730 to ABB05745 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polynucleotide encoding a cytokine receptor zcytor17 which useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maurer
                       transgenic
                                human rhinovirus;
                                                                 Human Ig-gammal heavy chain
                                                                                          22-FEB-2002
                                                                                                               AAM47856;
                                                                                                                                    AAM47856 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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29-JUN-2000;
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                               immunoadhesin; intercellular adhesion molecule;
rhinovirus; immunoglobulin heavy chain; J chain;
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                            NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                    PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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                                                                                                                                                                                       PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                     ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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2000US-214955P.
2001US-267963P.
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                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                       (first entry)
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97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention.
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                                                                  constant region amino acid
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Pred. No. 3.3e-90;
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    environment. Production is significantly less expensive in plants than animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a human immunoglobulin protein sequence, useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin has plant-specific glycosylation and virucide activity. The immunoadhesin is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 7; 138pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention.
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DB; ABA05265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                   ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                   NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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                                                                                                            ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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97.0%;
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Pred. No. 3.3e-90;
3; Mismatches 4
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: /cgn2_6/ptodata/1/pubpaa//SOR_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa//SOR_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa//SOR_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa//JSOR_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa//JSOR_PUBCOMB.pep:*
0: /cgn2_6/ptodata/1/pubpaa//JSOR_PUBCOMB.pep:*
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2: /cgn2_6/ptodata/1/pubpaa//JSOR_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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       US-09-847-208-3

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US-09-996-357-13

US-09-996-357-12

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US-10-47-542-20

US-09-995-898A-15

US-10-269-805-68

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                               Sequence 3, Appli
Sequence 7, Appli
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Sequence 10, Appl
Sequence 13, Appl
Sequence 18, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 14, Appl
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LENGTH: 232
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ALIGNMENTS

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Sequence 3, Application US/09847208

Publication No. US20030082190A1

GENERAL INFORMATION:

APPLICANT: SAXON, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
APPLICANT: Zhun, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67,002A

CURRENT APPLICATION NUMBER: US/09/847,208

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-09-847-208-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                  61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                    1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                       PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                            ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                              NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-09-847-208-2
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US-09-847-208-2
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                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                                                                                   SEQ ID NO 7
LENGTH: 569
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APPLICANT: Saxon, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
                                                                            Matches
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                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: 1gE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Saxon, Andrew APPLICANT: Zhang, Ke APPLICANT: Zhu, Daocheng
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                                                                                                                                                                     OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to OTHER INFORMATION: (IgE)
                                                                                                                                                                                                            ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                                                    TYPE: PRT
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hes 232;
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                                                                                            Similarity
                 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
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EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                                            100.0%;
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                                                                        Score 1260; DB 9;
Pred. No. 4.6e-88;
Mismatches 0;
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Pred. No 2.4e-88;
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; ORGANISM: Homo
US-09-996-357-10
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                                                                             Sequence 208, Application US/10207655 Publication No. US20030118592A1 GENERAL INFORMATION:
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APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BIOLING DOMAIN-IMMUNOGLOBULIN
FILE REFERENCE: 390069.401C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/250,198
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/257,186
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/996,357
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/253,302
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE
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97.0%;
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CURRENT APPLICATION

NUMBER: US/10/207,655

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LENGTH: 247;
TYPE: PRT;
ORGANISM: Homo sapiens
US-09-996-357-13
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APPLICANT: Gefter, Malcolm L
APPLICANT: Isreal, David I
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NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 208
LENGTH: 235
                                                                                                                                                          Query Match
Best Local Similarity
Matches .225; Conserv
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Best Local :
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CURRENT FILLING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/253,302
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/250,198
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/257,186
PRIOR APPLICATION NUMBER: 60/257,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE FILE REFERENCE; PPI-105
                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-12-20 NUMBER OF SEQ ID NOS: 13
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APPLICANT: Gosselin, Michael
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ORGANISM: Artificial Sequence
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al Similarity 97.08;
225; Conservation
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                                                 61 NWYVDGYEVHNYKTKPREEQYNSTYRVYSYLTVLHQNWMNGKEYKCKYSNKALPAPIEKT 120
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ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 135
                                                                                               Application US/09996357
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97.0%;
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Pred. No. 8e-86;
3; Mismatches
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; SEQ ID NO 6
rength: 251
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Best Local S
Matches 225
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CURRENT FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10152363A Publication No. US20030103986A1 GENERAL INFORMATION:
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APPLICANT: Xu, Wenfeng
APPLICANT: Henne, Randal M.
APPLICANT: Grant, Francis, J.
APPLICANT: Grant, Francis, J.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
FILE REFERENCE: 00-103
FILE REFERENCE: 00-103
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                     Query Match
                                                                                                                                                                                                        APPLICANT: Rixon, Mark W.
APPLICANT: Gross, Jane A.
TITLE OF INVENTION: TACT-Immunoglobulin Fusion
FILE REFERENCE: 01-20
CURRENT APPLICATION NUMBER: US/10/152,363A
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/293,343
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
  Best Local Similarity
                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                        TYPE: PRT
                                                                                  ORGANISM: Homo Sapiens
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97.0%; Pred. No. 8.2e-86;
tive 3; Mismatches 4
97.2%;
97.0%;
Score 1225; DB 9; Pred. No. 8.2e-86;
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 Sequence 14,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 12
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/250,198
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/257,186
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gosselin, Michael
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF
TITLE OF INVENTION: TREATING AN ANYLOIDOGENIC DISEASE
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CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/253,302
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PPI-105
                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                  156
                                                                                                                                             121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
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Application US/09822851B
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97.0%;
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Pred. No. 8.8e-86;
3; Mismatches 4
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GENERAL INFORMATION:
APPLICANT: Liu, Yang
APPLICANT: Diu, Xingl
APPLICANT: Zheng, Par
APPLICANT: Bai, Xue-F
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US-10-119-637A-14
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Best Local S
Matches 225
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                                                                                                                                                                                                                         SEQ ID NO 14
                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Methods of Blocking Tissue Destruction by Autoreative FILE REFERENCE: 22727/04117
CURRENT APPLICATION NUMBER: US/10/119,637A
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: 09/822,851
PRIOR PILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/192,814
PRIOR EFILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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LENGTH: 288
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                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/822,851B
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
                                                                                                                                          TYPE: PRT
ORGANISM: Artificial
FEATURE:
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                                                                               LOCATION: (1)..(52)
OTHER INFORMATION: mouse
                                                                                                  NAME/KEY: DOMAIN
LOCATION: (1)..(5
    OTHER INFORMATION:
                       NAME/KEY: DOMAIN LOCATION: (53)..
                                                              FEATURE:
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                                                                                                                                                                                                      LENGTH: 288
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225; Conserv
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                         . (55)
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sequence created by inventor; not from any
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97.0%;
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Pred No. 9.6e-86;
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known organism
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US-10-047-542-20
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; LOCATION: (56)..(288)
; OTHER INFORMATION: human IgG1
US-10-119-637A-14
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                                                                                                 QΥ
RESULT 13
US-09-995-898A-15
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SEQ ID NO 20
LENGTH: 330
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Best Local Similarity
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APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT APPLICATION NUMBER: DCT/US01/13932
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR APPLICATION NUMBER: PCT/US01/13932
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Similarity 97.0%;
25; Conservative
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                                                                                          PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                              ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                     PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
                                                                                                                                             ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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97.0%;
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Pred. No. 9.6e-86;
3; Mismatches 4;
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; ORGANISM: Homo sapiens
US-09-892-949-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 38, Application US/098 Publication No. US20030096339A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 15
LENGTH: 330
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APPLICANT: Presnell, Scott
APPLICANT: Xu, Wenfeng
APPLICANT: No. US200300277
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                                                       SEQ ID NO 38
LENGTH: 330
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                                                                                                                                                                                                                                                           TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: APPLICANT:
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APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/267,211
PRIOR FILING DATE: 2001-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE REFERENCE: 00-108
CURRENT APPLICATION NUMBER: US/09/995,898A
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
DELIG FILING DATE: 2000-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sprecher, Cindy A.
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                                                                                                                    PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
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                                                                                                   SOFTWARE: FastSEQ
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                                          TYPE: PRT
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Local Similarity 97.0%;
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Kuijper, Joseph L.
Maurer, Mark F.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Presnell, Scott R.
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Pred. No. 1 le-85;
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CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 330
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-269-805-68
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US-10-269-805-68
Sequence 68, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
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Best Local Similarity 97.0
Matches 225; Conservative
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Best Local 9
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TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
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219
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Pred. No. 1.1e-85;
3; Mismatches 4;
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Pred. No. 1.1e-85;
3; Mismatches 4;
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Search completed: July 15, Job time: 20.7984 secs

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Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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US-08-487-550-12
US-08-487-550-8
US-08-487-550-8
US-08-284-391B-33
US-09-218-950-33
US-09-318-950-33
US-09-318-950-33
US-08-887-352B-14
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US-08-887-352B-16
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US-08-887-352B-16
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US-09-180-100-22

US-08-784-512-3

US-09-176-228-3

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PCT-US95-03866-12

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PCT-US96-10043-9
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US-09-178-869-2
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US-08-236-311-7
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Sequence 22	US-08-146-206C-22	4	454	96.7	1219	
Sequence 22	US-08-437-642B-22	w	454	96.7	1219	w
Sequence 22	US-07-934-373C-22	N	454	96.7	1219	N
Sequence 18	US-09-301-593-18	4	453	96.7	1219	щ
Sequence 8,	US-08-466-163B-8	4	453	96.7	1219	0
Sequence 8,	US-08-466-151-8	ω	453	96.7	1219	39
Sequence 71	US-09-234-340A-71	4	452	96.7	1219	œ
Sequence 71	US-09-121-952A-71	4	452	96.7	1219	7
Sequence 71	US-09-026-985-71	4	452	96.7	1219	σ
Sequence 7,1	US-09-027-449-71	ω	452	96.7	1219	G
Sequence 18	US-09-296-005-18	4	451	96.7	1219	4
Sequence 16	US-09-296-005-16	4	451	96.7	1219	w
Sequence 14	US-09-296-005-14	4	451	96.7	1219	Ν
Sequence 2,	US-09-054-255-2	4	451	96.7	1219	1
Sequence 2,	US-09-282-505-2	4	451	96.7	1219	0
Sequence 18	US-09-109-207C-18	4	451	96.7	1219	9
Sequence 16	0S-09-109-20/C-16	4	401	. 96. /	FT7T	Q

ALIGNMENTS

Minimum

Maximum

Database

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RESULT 1
US-08-595-043A-50
; Sequence 50, Application US/08595043A
Patent No. 5935824
Patent No. 5935824
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             TELEFAX: (415)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SG.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                    TOPOLOGY: li
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61
                                                                                           EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                   NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                      EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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Length 360; Indels

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us-09-180-100-11
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US-09-178-869-2
                                                        EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 360
                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09180100 Patent No. 6306395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
LENGTH: 331
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: Wong, Shou
APPLICANT: Hickey, William F
APPLICANT: Hammang, Joseph P.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
ORGANISM: Homo sapiens 09-180-100-11
                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/180,100 CURRENT FILING DATE: 1998-11-02
                                                                                                                                                                                                                   APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/178,869B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEO ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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97.0%;
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US-08-236-311-7
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Best Local Similarity
                                                                                             TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/1 FILING DATE: 02-OCT-1987. ATTORNEY/AGENT INFORMATION: NAME: Hasak, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
FILING DATE: 18-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9:
FILING DATE: 26-AUG-1992
                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                    REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genen CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                FILING DATE: 28-SEP-1988 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 5.25 inch, 360 Kb floppy COMPUTER: IBM PC compatible OPERATIES SYSTEM: PC-DOS/MS-DOS
                      LENGTH: 3/1
TYDE: amino acid
                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                  FOPOLOGY:
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Pred. No. 2.1e-116;
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US-08-457-918-7
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                  NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
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APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                       FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2:
FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                           REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
                                                                                                                                                          PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 07/104329
                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
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 SEQUENCE CHARACTERISTICS:
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                         TELEPHONE: 415/225-04.
TELEFAX: 415/952-9881
TELEX: 910/371-7168
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                                                                                                     NAME: Kubinec, Jeffrey S. REGISTRATION NUMBER: 36,575
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                      FILING DATE:
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26-AUG-1992
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GENERAL INFORMATION:
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US-08-457-918-7
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                                    US-08-784-512-3
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Sequence 3, Application Patent No. 5872209
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09180100 Patent No. 6306395
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CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAKAMURA, No. 630
APPLICANT: NAGATA, Shigekazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE FILE REFERENCE: 1110-207P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 376
TYPE: PRT
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TOPOLOGY:
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97.0%;
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97.08;
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Pred. No. 2.2e-116;
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APPLICANT:

BARTNIK,

Eckart

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                          Sequence 3, Application Patent No. 6180334 GENERAL INFORMATION:
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Best Local :
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TELECOMMUNICATION INFORMATION: (202)672-5300
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FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
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TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: and native aggrecan to study the proteolytic
TITLE OF INVENTION: "Aggrecanase" in cell culture systems
APPLICANT:
              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 111
MOLECULE TYPE:
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FILING DATE: 17-JAN-
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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LOCATION:
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CTTY: Washington, D.C.
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                                                                                                                                                                                 READABLE FORM:
TYPE: Floppy disk
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Suite 500, 3000 K Street, N.W.
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EIDENMUELLER,
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BUETTNER, Frank
CATERSON, Bruce
              BARTNIK,
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linear
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              Eckart
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Pred. No. 2.4e-116;
3; Mismatches 4;
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PCT-US95-03866-12

Application PC/TUS9503866

Sequence 12, Applicat GENERAL INFORMATION:
APPLICANT: Cytome APPLICANT: Nocka,

CytoMed, Inc. (a

(all states JS only)

except US;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/176,228
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS: LENGTH: 396 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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FILING DATE: 17-JAN-1997
APPLICATION NUMBER: EP 9
                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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COMPUTER: IE
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NT: CATERSON, Bruce
NT: HUGHES, Clare
F INVENTION: An arti
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20007-5109
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PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 396
                  PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                            NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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Suite 500, 3000 K Street, N.W.
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97.0%;
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Pred. No. 2.4e-116;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                      Sequence 14, Application PC/TUS9503866 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                       APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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E: Fish & Neave
1251 Avenue of the Americas
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Pred. No. 2.7e-116;
3; Mismatches 4;
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PCT-US96-10043-11
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Query Match
Best Local Similarity
                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                     NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                               TELEPHONE: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: UFILING DATE: 28-MAR-
                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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Conservative
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             97.2%;
97.0%;
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             Score 1225; DB 5; Pred. No. 2.7e-116;
 Mismatches
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                           Length 424;
Indels
0;
Gaps
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Sequence 11, Application PC/TUS9610043 GENERAL INFORMATION: ZIP: 02210-2804 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C. APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Bolo-225 Franklin Street USA Version #1.30

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Best Local !
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                                                                                                                                                                                          ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 14-JUN-
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
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APPLICATION NUMBER:
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TELEFAX: 200154
                                                                         CLASSIFICATION:
                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                      CITY: Boston
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CLASSIFICATION:
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Similarity 97.0%;
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                                                                                                                                                                                                                                                                                                      225 Franklin Street
                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                         The General Hospital Corporation
VENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
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                  14-JUN-1995
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                                                                                                        PCT/US96/10043
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US-08-397-411-7; Sequence 7, A
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APPLICANT: Gingri
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SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                  STREET: UNE TO STREET: San Francisco
STATE: California
                                ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,
                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 27-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody
TITLE OF INVENTION: B-Cell Lymphoma and
                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: bi,
                                                                                                                                                              APPLICATION NUMBER: US/O FILING DATE: 01-MAR-1995
                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                            COMPUTER:
                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lech, Karen F. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weiner, George
                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bispecific Antibody Effective B-Cell Lymphoma and Cell Line
                                                                                                          us 07/859,583
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                                                                                                                                                                                   US/08/397,411
                                  30,223
                 011823-004901
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Pred. No. 2.8e-116;
""smatches 4;
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                                                                                                                                                                                                                        Version #1
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Best Local S
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                                           INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                       FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCUMEN: 30,223
                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Hun
TITLE OF INVENTION: GPI
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                                                                                          REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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ZIP: 9410
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TOPOLOGY: lin
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                                                                                         TELEPHONE:
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STRANDEDNESS:
                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                          ENGTH:
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225; Conserv
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5777085
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             amino acid
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One Market Plaza, Steuart
                          449 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                             415-326-2422
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97.0%;
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Pred. No. 2.9e-116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suite
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US-08-157-101A-7
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Best Local Similarity
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                                                                        TELEFAX: 202-822-0944
TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATION OPERATING SYSTEM: PC-DO SOFTWARE: Patentin Relaction DATA:
                                                                                                                   REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEPAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
MOLECULE TYPE:
                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 05-APR-1994
                            STRANDEDNESS:
                                             TYPE:
                                                                                                                                                                               NAME: TITUS, MARLANI
REGISTRATION NUMBER:
                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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               TOPOLOGY:
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5. 5808032
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                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                              D.C
                                                         459 amino acids
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TSURUOKA, NOBUO
                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KURIHARA, TATSUYA
MATSUKURA, SHIGEKAZU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NISHIHARA, TATSURO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARIMA, KENJI
                                                                                                                                                                                                                                                                                                    IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                 linear
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                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                            MARLANA K
peptide
                             single
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97.0%;
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                                                                                                                                                                  9437/204199
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Pred. No. 2.9e-116;
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                                                                                                                                                                                                                                                                                      Version
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Best Local Similarity

97.2%; 97.0%;

Score 1225; DB 1 Pred. No. 3e-116;

DB 1;

Length 459;

Query Match

Matches	225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	
Qy	1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60	
Db	228 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 287	
Qy	61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120	
Db	288 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 347	
Qy	121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180	
Db	348 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDTAVEWESNGQPENNYKTTP 407	
Оy	181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232	
Db	408 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 459	
search co	Search completed: July 15, 2003, 07:02:38	

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:52:29; Search time 18.5549 Seconds (without alignments) 1657.349 Million cell updates/sec

Title: Perfect score: Sequence: US-09-847-208B-6 1707 1 FTPPTVKILQSSCDGGGHFP.....HEAASPSQTVQRAVSVNPGK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	σ	ر.	4	ω	N		No.	Result
409	409.5	410	411.5	412	413	413.5	414	415	416	428	28.	0	1.1	39	439.5	55.	469	470	471	570	576	576	678.5	716	751	793	1644.5	1707	Score	
24.0			•	•	•	24.2	•	•	٠	٠	•	•	٠	•	•	•	27.5	•	•	•	33.7	33.7	•	•	•	46.5	٠	100.0	Match L	% Query
592	343	391	470	328	453	457	444	328	326	328	454	476	328	455	455	549	504	433	572	115	243	227	423	548	388	429	426	428	Length D	
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A; Molecule type: protein A; Accession: A94418

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	3 11	30
394	395.5	396	396.5	396.5	397	397.5	398	399	399	400.5	402	402.5	404	404.5	405.5
23.1	23.2	23.2	23.2	23.2	23.3	23.3	23.3	23.4	23.4	23.5	23.6	23.6	23.7	23.7	23.8
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G2MSAM	S31459	S01321	S14683	MHRBM	G1MSM	GHHU	S40295	S37483	G2MSA	147162	G1MS	MHHU	S15590	G2GP	MHRB
Ig gamma-2a chain	Ig gamma-1 chain -	Ig gamma-2b chain	Ig mu chain precur	Ig mu chain C regi	Ig gamma-1 chain C	Ig gamma-1 chain C	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma 4 chain c	Ig gamma-1 chain C	Ig mu chain C regi	Ig heavy chain - h	Ig gamma-2 chain C	Ig mu chain C regi

ALIGNMENTS

A; MOLECULE LyPE: INRAH A; RESIdues: 1-428 \CSEN\ A; Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035 A; Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035 A; Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035 A; Cross-references: Apublication and deletion in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference number: Apublication in the human immunoglobulin epsilon genes. A; Reference n	A;Accession: PH1214 A;Accession: PH214 A;Accession: PH214 A;Accession: PH214 A;Accession: PH214 A;Accession: PH214 A;Accession: PH214 A;Accession: M20-428 < ZIAA> A;Residues: 320-428 < ZIAA> A;Cross-references: EMBL:X63693; GB:S38668; NID:g32987 A;Cross-references: EMBL:X63693; GB:S38668; NID:g32987 A;Cross-references: EMBL:X63693; GB:S38668; NID:g32987 A;Accession: Accession: Acces	EMBO SALIMATED AND AND AND AND AND AND AND AND AND AN	RESULT 1 EHHU Ig epsilon chain C region - human C:Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999 C:Accession: A22771; A33195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; R:Flanagan, J.G.; Rabbitts, T.H. EMBO J. 1, 655-660, 1982 A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region g A:Reference number: A22771; MUID:84236029; PMID:6234164 A:Accession: A22771 A:Molecule type: DNA A:Residues: 1-428 <fla> A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035 A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035</fla>
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A,Cross-references: GDB:119335; OMIM:147180
A;Map position: 14932.33-14932.33
A;Introns: 1/1; 104/1; 211/1; 319/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog F;22-87/Domain: immunoglobulin homology <IM2>
E;128-195/Domain: immunoglobulin homology <IM2>
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C; Geneti
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A; Residues: 320-428 <ARE>
A; Residues: 320-428 <ARE>
A; Experimental source: myeloma U266-derived cell line AF-10
A; Note: sequence extracted from NCBI backbone (NCBIN:141701,
R; Hellman, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 382-426 <HEL>
A;Cross-references: GB:S55273; NID:9263166; PIDN:AAB24857.1; PI
A;Experimental source: B cell myeloma U-266
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R;Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts
A;Reference number: A53116; MUID:94103254; PMID:8276835
A;Accession: A53116
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A;Title: Cloning and sequence determination of the gene for the human immur A;Reference number: A93933; MUID:83065234; PMID:6815656
A;Accession: B93933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:S53497; NID:g263162; A;Experimental source: B cell myeloma U-266
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A; Residues: 401-428 <HE3>
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A;Residues: 382-391 (HE2>
A;Cross-references: GB:S55276; NID:g263168;
A;Experimental source: B cell myeloma U-266
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A; Accession: D46536
A; Status: preliminary; not compared with conceptual translation
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A; Residues: 1-40;68-114;427-428
A; Cross-references: GB:L00022; 1
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                                                                                   ;128-195/Domain: immunoglobulin homology <IM2>;332-301/Domain: immunoglobulin homology <IM3>;332-301/Domain: immunoglobulin homology <IM4>;338-407/Domain: immunoglobulin homology <IM4>;138-407/Domain: immunoglobulin homology <IM4>;14/Disulfide bonds: interchain (to light chain) #status predicted ;15-105,29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted ;21,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status ;121,209/Disulfide bonds: interchain (to heavy chain) #status predicted
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PMID:8419166
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   DB 1;
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rroc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A; Title: Nucleotide sequences of immunoglobulin epsilon
A; Reference number: I36948; MUID:87147196; PMID:3103123
A; Accession: I36948
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C; Superfamily: imn
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c;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: 136948...
R;Sakoyama, Y:; Hong, K.
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A; Residues: 1-426 < RES>
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                                                                                                                                                                                               LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
HEAASPSQTVQRAVSVNPGK
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                                                    NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                                                                                                                                                                                                FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                     RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                          LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                                                         GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
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                                      NEMPEDISVQWLHNEVQLPDARHSTTQPHKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                         RDWIEGETYQCRVTHPHLPRALVRSTTKTSGPRAAPEVYAFATPEGPGSRDKRTLACLIQ
                                                                                                                                             LF IRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKQEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                                                                                   FT-PTVKVLQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASATQE
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97.2%;
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R;Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T. Nucleic Acids Res. 10, 6041-6049, 1982
A;Title: Structure and evolution of the heavy chain from A;Reference number: A93442; MUID:83064537; PMID:6292865
A;Accession: A93442
                                                              EHMS
Ig epsilon chain C region (version 1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C;Accession: A02144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;118-186/Domain: immunoglobulin homology <IM2>F;223-291/Domain: immunoglobulin homology <IM3>F;327-398/Domain: immunoglobulin homology <IM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 'N',169-307,'L',309-342 <KIN>
A;Residues: 'N',169-307,'L',309-342 <KIN>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaphain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication: glycoprotein; heterotetramer; immunoglobulin
C;Keywords: duplication: glycoprotein; heterotetramer; immunoglobulin
E;19-80/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A9093
A; Contents: myeloma IR162
A; Accession: A90937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, A; Reference number: A90937; MUID:83182019; PMID:6820340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig epsilon chain C region - rat C:Species: Rattus norvegicus (Norway rat) C:Species: 17-Dec-1982 #text_change 16-Jul-1999 C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999 C:Accession: A93442; A90937; A02143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-429 <HEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
                    R;Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H. Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKPTVDLLHSSCDPNA-FHSTIQLYCFVYGHIQNDVSIHWLMDDRKIYETHAQNVLIKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 180
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                                                                                                                                                                                                                                       VIHEALREPRKLERTISKSLG 418
                                                                                                                                                                                                                                                                             AVHEAASPSQTVQRAVSVNPG 319
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                                                                                                                                                                                                                                                                                                                                                                                                            KDWIEGEGYQCRVDHPHFPKPIVRSITKAPGKRSAPEVYVFLPPE-EEEKDKRTLTCLIQ
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and nucleotide
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  sequence
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Pred. No. 1.1e-51;
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  of
f
  mouse
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immunoglobulin
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A; Residues: 1-548 < KIP>
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KLNITEQQWMSESTFTCKVTSQGVDYLAHTRRCPDHEPRGVITYLIPPSPLDLYQNGAPK 357
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-388 < LIU>
A; Residues: 1-388 < LIU>
A; Cross-references: GB: J00476; NID: g194875; PIDN: AAA38085.1; PID: g387220
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 81-44/Domain: immunoglobulin homology (fragment) < IM1>
F; 81-149/Domain: immunoglobulin homology (fragment) < IM1>
F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, Nove A;Description: Combination of a defined A;Reference number: $38864 A;Accession: $38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig epsilon chain C region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
C;Accession: S38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;186-254/Domain: immunoglobulin homology <IM3>
F;290-361/Domain: immunoglobulin homology <IM4>
F;10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status
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                                                                                                                      238 FPPKPKDVLTRSTIQLYCFIYGHILNDVSVSWLMDDREITDTLAQTVLIKEEGKLASTCS
69 ELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFDLFIRKSPT
                                                                                                                                                                                                                                                                                                               Similarity 45.0
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKLASTCSKLNITEQQWMSESTFTCKVTSQGVDYLAHTRRCPDHEPRGVITYLIPPSPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEPTLELLHSSCDPNA-FHSTIQLYCFIYGHILNDVSVSWLMDDREITDTLAQTVLIKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIHEALQKPRKLEKTISTSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVHEAASPSQTVQRAVSVNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEMPEDISVOWLHNEVQLPDARHSTTQPRKTKGS--GFFVFSRLEVTRAEWEQKDEFICR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFFPEDISVQWLGDGKLISNSQHSTTTPLKSNGSNQGFFIFSRLEVAKTLWTQRKQFTCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYQNGAPKLTCLVVDLESEK-NVNVTWNQEKKTSVSASQWYTKHHNNATTSITSILPVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schlaak, M.
                                                                                                                                                                                                                                                                                                                                                         41.9%;
45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.0%; Score 751; DB 1;
45.8%; Pred. No. 1.3e-48;
                                                                                                                                                                                                                TIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTTQEGELASTQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C region; immunoglobulin homology lin homology <IMM>
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                                                                                                                                                                                                                                                                                                               56;
                                                                                                                                                                                                                                                                                                                                                     Score 716; DB 2;
Pred. No. 8.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            November 1993
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                                                                                                                                                                                                                                                                                                                                                                                          Length 548;
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                                                                                                                                                                                                                                                                                                          Indels
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C;Genetics:
A;Introns: 91/1; 199/1; 307/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical lig c;Complex: An immunoglobulin heterotetramer subunit consists of two identical lig c;Complex: An immunoglobulin c some cases, such as IgA and IgM, the subunits associate C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;16-77/Domain: immunoglobulin homology <IMMI>
    밁
                                         Qy
                                                                                        В
                                                                                                                           Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig epsilon chain C region (version 2) - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 C;Accession: A02145
                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ωy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
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A; Residues: 1-423 <I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;115-183/Domain: immunoglobulin homology <IMM2>;220-288/Domain: immunoglobulin homology <IMM3>;325-396/Domain: immunoglobulin homology <IMM4>;325-396/Domain: immunoglobulin homology <IMM4>;325-396/Domain: immunoglobulin homology <IMM4>;23-75,122-181,227-286,332-394/Disulfide bonds: #status;43,84,167,239,262,417/Binding site: carbohydrate (Asn)
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                                                                                                                                                                                                                                                                                                                                                                   72 LSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFDLFIRKSPTITC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-423 <ISH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
    KLEKTISTSLG 416
                                                                                                                                                                                                                                                                                                                                         TEQQWMSESTFTCRVTSQGVDYLAHTRRCPDHEPRGAITYLIPPSPLDLYQNGAPKLTC
                                                                                                                                                                       VVDRPDFPKPIVRSITLPQVSQRSAPEVYVFPPPE-EESEDKRTLTCLIQNFFPEDISVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDGGGHFPPTIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTTQEGELASTQSELT 71
                                                                                   WLGDGKLISNSQHSTTTPLKSNGSNQGFFIFSRLEVAKTLWTQRKQFTCQVIHEALQKPR
                                                                                                                             WLHNEVQLPDARHSTTQPRKTKGS--GFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQ
                                                                                                                                                                                                                 RVTHPHLPRALMRSTTKTS-GPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQ 250
                                                                                                                                                                                                                                                         LVVDLESEK-NVNVTWNQEKKTSVSASQWYTKHHNNATTSITSILPVVAKDWIEGYGYQC
                                                                                                                                                                                                                                                                                    LVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQC 191
                                                                                                                                                                                                                                                                                                                                                                                                                             CDPNA-FHSTIQLYCFIYGHILNDVSVSWLMDDREITDTLAQTVLIKEEGKLASTCSKLN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRKLEKTISTS 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQWLHNEVQLPDARHSTTQPRKTKGS--GFFVFSRLEVTRAEWEQKDEFICRAVHEAASP
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                                              TVQRAVSVNPG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoglobulin heterotetramer subunit consists of two identical light
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTCLVVDLESEK-NVNVTWNQEKKTSVSASQWYTKHHNNATTSITSILPVVAKDWIEGYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YQCIVDHPDFPKPIVRSITKTPGQRSAPEVYVFPPPE-EESEDKRTLTCLIQNFFPEDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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43.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 678.5; DB 1
Pred. No. 3.7e-43;
5; Mismatches 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PH1216
If epsilon chain C region form N; Alternate names: Ig epsilon c N; Alternate name saniens (man)
Db
                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin A;Reference number: A53116; MUID:94103254; PMID:8276835 A;Accession: D53116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Exp. Med. 176, 233-243, 1992
A;Title: Two unusual forms of human immunoglobulin E encoded A;Reference number: PH1214; MUID:92308839; PMID:1613458
A;Accession: PH1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: Ig epsilon chain C region, membi
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
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C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change 21-Jan-2000
C;Accession: PH1215
                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-243 <ZH2>
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A; Residues: 1-243 < ZHA>
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J. Exp. Med.
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A; Residues: 1-227 < ZHA>
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A;Title: Two unusual forms of human immunoglobulin E encoded A;Reference number: PH1214; MUID:92308839; PMID:1613458
A;Accession: PH1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Zhang, K.;
J. Exp. Med.
                                                                                                                                                                                                                                   A; Introns: 108/1
                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                             A; Note: sequence extracted
                                                                                                                                                                                                                                                                                                 A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X63693
R;Zhang, K.; Max, E.E.; Cheah, )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 108/1; 200/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem.
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Best Local S
Matches 108
                                                                                                                                                            Superfamily: immunoglobulin C region; Keywords: alternative splicing; immuno;19-88/Domain: immunoglobulin homology
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PRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT
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269, 456-462, 1994
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llarity 100.0%;
Conservative
                                                                                   Conservative
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chain C region, membrane-bound
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                                                                               Score 576; DB 2; .; Pred. No. 8.3e-36; ...
                                                                                                                                                                                         immunoglobulin
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                                                                                                                         Length 243,
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NCBIN: 141711,

NCBIP: 1417

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produ

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Gaps

0

60 271 bу

alternative

RNA

splic

form (clone CH4-M2')

21-Jan-2000

108

0;

Gaps

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60

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Ay I meavy chain (7.85) - duck

N;Alternate names: Ig gamma chain (7.85)

C;Species: Anas platyrhynchos (domestic duck)

C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C;Accession: B46529; S20759

R;Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.

J. Immunol. 149, 2627-2633, 1992

A;Title: Structural relationship between the two Igy of the duck, Anas platyrhynchos:
A;Reference number: A46529; MUID:93017865; PMID:1401901

A;Accession: B46529

A;Status. ~~~15-
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J. Biol.
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A; Residues: 1-572 <MAG>
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A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin A;Reference number: A53116; MUID:94103254; PMID:8276835
A;Accession: E53116
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C;Species: Homo sapiens (man)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994
C;Accession: E53116
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A; Residues: 1-115 <ZHA>
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                                                                                                                  TPPEVQVLHSSVCSTLG--DDSVELLCVITGFSPPPVEVEWLVDG--APAHLVATMTRPQ
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                                                                             GELAS ----TQSELTLSQKHWLSDRTYTCQVTY --QGHTFEDSTKKCADSNPRG---VSA
                                                                                                                                                         TPPTVKILQSS-CDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                      REAGSKTYMATSQTNVSREDWKAGKAFTCRVKHPATGGTAQGHARFCPGSGAQSCSPIQI
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YLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLT
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32.0%;
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                                                                                                                                                                                             Mismatches 141;
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S31436
                                                                       Ig gamma chain (clone 36) - chicken (fr
N;Alternate names: Ig nu chain
C:Species: Gallus gallus (chicken)
C:Date: 07-Sep-1990 #sequence_revision
C:Accession: S00390
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S00390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig upsilon chain - axolotl (fragment)
c;Species: Ambystoma mexicanum (axolotl)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Accession: S31436
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A; Residues: 1-433 <FEL>
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A; Title: Chicken imm
A; Reference number:
                                    R;Parvari, R.; Avivi, A.; Lentner, F.; Ziv, E.; Tel-Or, S.; Burstein, Y.; Schechter, EMBO J. 7, 739-744, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 31.(
)2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KARDLYIANQPVVICKITKMENS-DSLSVTWKRREGPEEAAVISEQYIDSDGTFTAMSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GE-LASTQSELTLSQKHWLSDRTYTCQVTYQGHT--FEDSTKKCADS-NPRGVSAYLSRP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQP-RKTKGSG-FFVFSRLEVTRAEW 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: ||| |:||: : ||||:| || :::::|:|
EVVPPSPGSLXIRQDAKVHCLVVNL-PSDASLSISWTREKSGALRPDPMVLTEHFNGTFT
                                                                                                                                                                                                                                                                                             KDEFICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                NITKNEWERGDEFTCKVKHFDLPFPLSRSVSKPTGRSFAPTMYVFAPHEMELANYDFVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQGTFSTTSQINVTKSDWASGDKYTCKVEHPATSSRAEDTIHNCADSQTPYQPKVFLIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGGVSYACMVVHEGL-PMRFTQRPLQKTPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASSSLAISTODWLAGERFTCTVQHEDLPVPLGKSIAKHAGKVTAPYIFTFPPHAEELSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRD
                                                                                                                                                                                                                                                                                                                                                                       ACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSG----FFVFSRLEVTRAEWEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWP-GSRDKRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQKDEFICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                         RETFTCVAAHSAV-PKNLMTRRIQKPLGK
                                                                                                                                                                                                                                                                                                                                    TCLVKSFSPDDIYIQWKQGKSVIPSDKYVSMEPRQEAGTAGLGTYFSYSMLTIQKSDWDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVTLTCLVRGFQPEHVEVQWLRNHNSVPAAEFVTTPPLKEPNGDGTFFLYSKMTVPKASW
immunoglobulin
er: S00390; MUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.5%;
  MUID:88283642;
gamma-heavy chains: limited VH
D:88283642; PMID:3135182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 470;
Pred. No. 1.
                                                                                                                                                         (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                             07-Sep-1990 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
..3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 18;
                    gene repertoire, combi
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A:Residues: 'LC',3-308,'H',310-549 <LIT>
A:Residues: 'LC',3-308,'H',310-549 <LIT>
A:Cross-references: EMBL:X15114; NID:g64799; PID:g763031
C:Superfamily: immunoglobulin C region; immunoglobulin hc
C:Keywords: glycoprotein; heterotetramer; immunoglobulin
F:26-109/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, A; Reference number: S05695
A; Accession: S05695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain precursor - African clawed frog (fragment) C;Species: Xenopus laevis (African clawed frog) C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change C;Accession: S04845; S05695 R;Amens, G.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
S04845
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A; Residues: 1-549 < AME>
A; Cross-references: EMBL:X15114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 17, 5388, 1989
A;Title: Nucleotide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin A;Reference number: S04845; MUID:89345103; PMID:2503814
A;Accession: S04845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S00390
A;Molecule type: mRNA
A;Residues: 1-504 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Litman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: X07174
                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                      294/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity
108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PTVKILQ-SSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                                                                                                                                                                                                     Similarity
     LASTQSELTLSQKHWLSDRTYTCQVTY-QGHT-FEDSTKKCADSNPRGVSAYLSRPSPFD 120
                                                                           PTVEILQGPCASS----KSVELLCLITGYAPSEIKVHWLLNGQVTNISPSNSKPCKEENG
                                                                                                                      PTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTAS-TTQEGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLIQNFMPEDISVQWLHNEVQLPDARHSTT----QPRKTKGSG----FFVFSRLEVTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPGELYISLDAKLRCLVVNL-PSDSSLSVTWTREKSGNLRPDPMVLQEHFNGTYSASSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KWNGGTVFACMAVHEAL-PMRFSQRTLQKQAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLVRGFRPRDIEIRWLRDHRAVPATEFVTTAVLPEERTANGAGGDGDTFFVYSKMSVETA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVSTQDWLSGERFTCTVQHEELPLPLSKSVYRNTGPTTPPLIYPFAPHPEELSLSRVTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYSLSSRVNVSGTDWREGKSYSCRVRHPATNTVVEDHVKGCPDGAQSCSP--IQLYAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LASTQSELTLSQKHWLSDRTYTCQVTY - - QGHTFEDSTKKCADS - - - - NPRGVSAYLSRP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEVQVLHASSCTPSQ--SESVELLCLVTGFSPASAEVEWLVDGVGGLLVASQSPAVRSGS
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                  26.7%;
33.0%;
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Pred. No. 1.9e
60; Mismatches
                                                                                                                                                                                                  Score 455.5; DB 2
Pred. No. 2.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             April
                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .9e-27;
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                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                           Indels
                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                           549;
                                                                                                                                                                         15;
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                                                                           295
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F;129-201/Domain:
F;239-307/Domain:
F;346-417/Domain:
                                                                    C;Keywords: alternative splicing; duplication; glycoprotein;
F;21-91/Domain: immunoglobulin homology <IMM1>
                                                                                                               C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 1-77,'N',79-100,'Q',102-225,'N',227-257,'T',259-367,'K',369-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-225,'N', 227-257,'S', 259-367,'K', 369-455 <AUF>
R; Kehry, M.; Sibley, C.; Fuhrman, J.; Schilling, J.; Hood,
Proc. Natl. Acad. Sci. U.S.A. 76, 2932-2936, 1979
A; Reference number: A26241; MUID:79223904; PMID:111247
A; Contents: annotation; MOPC 104E
                                                                                                                                                                      A;Introns: 1/1; 106/1; 219/1; 325/1 C;Complex: An immunoglobulin hetero
                                                                                                                                                                                                                                                                                             A; Accession: B02039
                                                                                                                                                                                                                                                                                                                                           A; Title: Complete amino acid sequence of a A; Reference number: A02039; MUID:83075344;
                                                                                                                                                                                                                                                                                                                                                                                        A; Note: this sequence has been revised in reference A02039. Carbohydrate binding R; Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L. Biochemistry 21, 5415-5424, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Nucleotide sequence of a cloned cDNA corresponding A; Reference number: A26240; MUID:81165562; PMID:6260591 A; Contents: TEPC183
                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                    A; Contents: MOPC 104E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A26240
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immunoglobulin homology <IMM2>
immunoglobulin homology <IMM3>
immunoglobulin homology <IMM4>

heterotetramer;

immunogi

mouse mu chain: PMID:6816276

homology

among

heavy chain

site

L.E

ç

secreted

∄u

chain

of.

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A; Molecule type: DNA
A; Residues: 1-455 <GOL>
A; Note: the sequence was
                                                                                 A;Reference number: A26239; MU
A;Accession: A26239
A;Molecula +---
                                                                                                                                                                                                                                                                       Nucleic Acids Res. 8, 3933-3945, 1980
A;Title: Complete nucleotide sequence of mouse immunoglobulin A;Reference number: A02166; MUID:81076590; PMID:6255422
A;Accession: A02166
R; Auffray, C.; Rougeon, F. Gene 12, 77-86, 1980
                                                                                                                                                       Gene 15,
                                                                                                                                                         R;Goldberg, G.I.; Va
Gene 15, 33-42, 1981
                                                                                                                                                                       A; Note: the sequence was determined from the germline R; Goldberg, G.I.; Vanin, E.F.; Zrolka, A.M.; Blattner,
                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change
C;Accession: A02166; A26239; A26240; B02039
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                                                                                                                                    A; Title: Sequence of the
                                                                                                                                                                                                                  A; Cross-references: GB:J00443
                                                                                                                                                                                                                                    A; Molecule type: .DNA
A; Residues: 1-455 <KAW>
                                                                                                                                                                                                                                                                                                                                                         R;Kawakami,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHEAASPSQTVQRAVSVNPGK 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDWIEGETYOCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLVTKEAKVYCVISRMA-STDDLTVQWSRSDGKKALAFDSAPEKAYDGTFTVKSTLKISP 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFRPQDIYVFWKKDGVTLEEDYYMTTTPVLEEEEEGFISFSKLTIARSDWMRGATYSCIA
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                                                                                                                                                                                                                                                                                                                                  Takahashi, N.; Honjo,
es. 8, 3933-3945, 1980
                                        determined from the
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                                      germline gene
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F:28-89/Disulfide bonds: #status experimental
F:46,211,243;281,442/Binding site: carbbhydrate (Asn) (covalent) #status experimental
F:136-199,246-305,353-415/Disulfide bonds: #status predicted
F:216,454/Disulfide bonds: interchain (to me chain in another subunit) #status predicted
F:293/Disulfide bonds: interchain (to me chain in another subunit) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:X03690; NID:g52381; PIDN:CAA27326.1; PID:g52382
A;Experimental source: strain C57BL/6
A;Note: the authors translated the codon AAG for residue 65 as Leu C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin C region; C;Keywords: immunoglobulin F;346-417/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ωy
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                                                                                                                                              δÃ
                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 14, 2381-2389, 1986
A;Title: Allotypic differences in murine mu-genes.
A;Reference number: A24976; MUID:86176735; PMID:3083402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Schreier, P.H.; Quester, S.; Bothwell, A.
     B 6
                                                                                                В
                                                                                                                                                                                                                                            Qy
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A; Residues: 1-455 <SCH>
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                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 106
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Best Local S
Matches 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 PNVNVFVPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENK 171
                                              117 SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                     172 GSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLTFLKNVSSTCAASPSTDILTFTIPP
                                                                                                                                                                                                     112 PNVNVFVPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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106; Conserv
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                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LASTQ-----SELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVCVEDWNNRKEFVCTVTHRDLPSPQKKFISKPNEVHKHPPAVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP--EWPGSRDKRT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFADIFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPNGTFSAKGVA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETYTCVVGHEAL-PHLVTERTVDKSTGK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTVKILQSSCDG-GGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
SFADIFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPNGTFSAKGVA 290
                                                                                                                                                                                                                                                 PTVKILQSSCDG-GGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTHSILTVTEEEWNSG 410
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32.3%; Pred. No. 2.7e
tive 57; Mismatches
                                                                                                                                                                                                                                                                                                25.7%; score 439.5; DB 2; 32.3%; Pred. No. 2.7e-25; tive 57; Mismatches 152;
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ches 152;
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                                                                                                                                                                                                                                                                                                                                                 Length 455;
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                                                                                       LACLIQNEMPEDISVOMLHNEVQLDDARHSTTQPRKTKGS-GF-FVFSRLEVTRAEWEQK 292
                                                                                                                                                                    PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP--EWPGSRDKRT
                                                                                                                                             SYCVEDWNNRKEFYCTYTHRDLPSPQKKFISKPNEVHKHPPAVYLLPPAREQLNLRESAT
ETYTCVVGHEAL-PHLVTERTVDKSTGK 437
                                  DEFICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                      VTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTHSILTVTEEEWNSG 410
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Search completed: July 15, 2003, 06:59:32 Job time: 19.5549 secs

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Result
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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PROSITE; PS00290; IG_MHC
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"A model of the Fc of immunoglobulin E.";
Mol. Immunol. 23:1063-1075(1986).
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P01855;
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MEDLLINE=82174576; PubMed=6803328;
Hellman L., Pettersson U., Bennich H.;
"Characterization and molecular cloning of the mRI
(epsilon) chain of rat immunoglobulin E.";
Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A cloned cDNA probe for rat a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=LOU/C/WSL;
MEDLINE=83064537; PubMed=6292865;
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Mammalia; Eutheria; Rodentia;
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21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation rig epsilon chain C region.
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SM00407; IGC1; 1.
E; PS00290; IG_MHC; 3.
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                                    GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
GKLASTYSRLNITQQQWMSESTFTCKVTSQGENYWAHTRRCSDDEPRGVITYLIPPSPLD
                                                                                        TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTTQE
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54; Mismatches
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Sciurognathi; Muridae; Murinae; Rattus.
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P06336; P01856;
21-JUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence upda
15-JUL-1999 (Rel. 38, Last annotation up
19 epsilon chain C region.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Rodentia; Sciurognat
NCBL_TaxID=10090;
                                         InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_cl.
InterPro; IPR003507; Ig_like.
Pfam; PF00047; ig; 4.
SMARF; SM00410; IG_like; 2.
SMART; SM00407; IGCl; 2.
PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin domain; Immunog
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Immunoglobulin on NON_TER 1
DOMAIN 1
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                                                                                                                                                                                           EMBL;
EMBL;
PIR; /
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Liu F.-T., Albrandt K., Sutcliffe
"Cloning and nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF
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Sciurognathi;
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RA Kawakami T., Takahashi N., Honjo T.;
RT "Complete nucleotide sequence of mouse immunoglobulin mu (comparison with other immunoglobulin heavy chain genes.";
Nucleic Acids Res. 8:3933-3945(1980).

[2] SEQUENCE FROM N.A.

MEDLINE-Pagaria
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Ig mu chain C region
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P01872;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
             SEQUENCE FROM N.A.

MEDLINE=82051295; PubMed=6795090;

Goldberg G.I., Vanin E.F., Zrolka

"Sequence of the gene for the cons

Balb/c mouse immunoglobulin.";

Gene 15:33-42(1981).
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-i- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LY SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SE THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER
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Kehry M.R., Sthilling J.
Wahino acid sequence of a mouse immunoglobulin mu
Panino acid sequence of a mouse immunoglobulin mu
Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979).
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EMBL; V00821; CAA24202.1; PIR; A02167; MHMSM.
                                                                       use
                                   or send
                                                                                    the
                                                                                                                                                                                                 forms of immunoglobulin mu chain. Cell 20:303-312(1980).
-!- ALTERNATIVE PRODUCTS: DURING
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MEDLINE-80222874; PubMed-6771020;
POGRAFA J. Davis M., Calame K.,
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
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5-JUL-1999 (Rel. 38,
5 mu chain C region I
Is musculus (Mouse).
                                                                                  ween the Swiss Institute of Bioinfo
European Bioinformatics Institute.
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Ol-JAN-1988 (Rel. 06, Created)
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15-JUL-1999 (Rel. 38, Last annotation updat Ig mu chain C region.
Mesocricetus auratus (Golden hamster).
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SMART; SM00407; IGcl; 2.
                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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"Phylogenetic conservation of immunoglobulin
comparison of hamster and mouse Cnu genes.";
Nucleic Acids Res. 13:5611-5628(1985).
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                                                 LILRESATVTCLVKGFSPADIFVQWLQRGQPLSQDKYVTSAPMREPQAPHLYFTHSVLTV
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MEDLINE-9525598; PubMed=; Stoppini M., Bellotti V., "Characterization of the timmunoglobulins."; Eur. J. Rich
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Can. J. Biochem. 57:758-767(1979).
[6]
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21-JUL-1986
16-OCT-2001
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Hofmann T., Parr D.M.;
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immunoglobulins gamma chains.";
immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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MEDIIND-83001943; PubMed=6811139;
MEDIAND-83001943; PubMed=6811139;
MEDIAND-83001943; PubMed=6811139; Ni
Takahashi N., Ueda S., Obata M., Ni
"Structure of human immunoglobulin
evolution of a gene family.";
Cell 29:671-679(1982).
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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MEDLINE=84235992; P
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Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
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Bellotti V., Negri A.,
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C -> S (IN REF.
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SMART; SM00407; IGCl; 3.
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"Nucleotide sequence of Suncus murinus immunoglobulin
comparison with mouse and human mu genes.";
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Mammalia; Eutheria; Insectivo
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PIR; S03961; S03961.
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ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                    PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
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PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIEVSWLREGK----QVGSGVTTDEVE
                                                                                                                                                              PS00290; IG_MHC; 3.
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43
156
262
391 /
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40,
                                                                                                                                                                                                                                                                                                                                                                                                                                disease
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S., Mihaesco E.,
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Ig_c1.
Ig_like
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Last sequence update)
Last annotation updat
                                                                                                                                                  Immunoglobulin
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                                           b; Score 410; DB
b; Pred. No. 1.3e
61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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                                                                                       Inoglobulin C region.

PRE-C-PART (NO V REGION HO
CH2.
CH3.
CH4.
9100843AF0CF021A CRC64;
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                                                                                                                                       HOMOLOGY).
                                                                   391;
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Nucleic
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P01871;
21-JUL-1986
01-FEB-1991
15-JUN-2002
Ig mu chain
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90332450; PubMed-2115996; Friedlander R.M., Nussenzweig M.C., "Complete nucleotide sequence of the heavy chain.";
                                                                                                                                                                                                            "The
                                                                                                                                                                                                                                                                         Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.; "The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain type), subgroup H III. Architecture of the complete IgM-molecule. Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
SEQUENCE
                                                                 PARTIAL SEQUENCE FROM N.A. MEDLINE-82059479; PubMed-6795593;
                                                                                                    Science
                                                                                                                "Complete amino acid sequence immunoglobulin.";
                                                                                                                                                SEQUENCE (WALDENSTROM'S OU), DISULFIDE MEDLINE=74005511; PubMed=4742735;
                                                                                                                                                                                               protein
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MEDLINE-81066716;
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                                             "Human
                                                                                                                                        Putnam F.W., Florent
                                                                                                                                                                                                                      Hilschmann N.
                                                                                                                                                                                                                                                                                                                                    SEQUENCE (WALDENSTROM'S MACROGLOBULIN MEDLINE=75059123; PubMed=4803843;
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ein BOT.":
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                    immunoglobulin heavy chain genes:
C delta and C gamma genes and assoc
C Acids Res. 9:4509-4524(1981).
                                                                                                                                                                                                BOT.
                                                                                                    182:287-291(1973)
                                                                                                                                                                                    Biochem.
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OF,
                                                       T.H., Forster A., Milstein C.P.;
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(Rel. 17,
(Rel. 41,
Cregion.
299-387
                                                                                                                                                                                                                               6716; PubMed=6777162; Barnikol-Watanabe S.,
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                                                                                                                                                                                 111:275-286(1980).
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17,
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AND
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438-454
                                                                                                                          C., Shinoda T.,
of the Mu heavy
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; Ig; 4.
SMART; SM00407; IG; 18; 1.
SMART; SM00407; IGc1; 3.
PROSITE; PS00290; IG_MHC; 3.
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"Cloning and partial nucleotide sequence of human immunoglobulin mu
"chain cDNA from B cells and mouse-human hybridomas.";

Proc. Natl. Acad. Sci. U.S.A. 77:6027-6031(1980).

-!- MISCELLANEOUS: ALL 4 COMBINATIONS OF THE S/G & V/G POLYMORPHISMS
AT POSITIONS 192 AND 216 HAVE BEEN OBSERVED IN HUMAN MU CHAINS.
                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlycoSuiteDB; P01871;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X17115; CAA34971.1; ALT_SEQ EMBL; X57086; -; NOT_ANNOTATED_CD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long a
modified and this statement is not removed;
entitles requires a license agreement (See i
or send an email to license@isb-sib.ch).
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                                                                                                                             Similarity
                                                                             PRVSVFVPPRDGFFGNPRSKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEA
PSFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGE
                                        KESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIP
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                   PSPFDLF IRKSPT ITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
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28.6%;
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                                                                                                                      64;
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Pred. No. 3.5e
54; Mismatches
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N-LINKED
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V -> G
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S -> G
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15 mu chain C region.
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"Complete sequence of a cloned cDNA encoding rabbit secreted mu-c
of VHa2 allotype: comparisons with VHa1 and membrane mu sequences
J. Immunol. 132:490-495(1984).

-1- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES
SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF
THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                          CARBOHYD
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SMART; SM00407; IGC1; 2.
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MEDLINE=84088930; PubMed=6418803;
Bernstein K.E., Alexander C.B., Reddy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9986;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
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RESULT 12
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SEQUENCE OF 134-226.

MEDLINE=75036072; PubMed=4429665;

Tracey D.E., Cebra J.J.;

"Primary structure of the CH2 hom antibodies.";
                                                                   Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guilimmunoglobulin-G(2). II. Amino acid sequence and hinge region cyanogen bromide fragments.
Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                             immunoglobulin-G(2). 3. Amino acid sequence half-cystine joining heavy and light chains. Biochemistry 10:18-25(1971).
                                                                                                                                                                                              Birshtein B.K., Hussain Q.Z., Cebra J.J., "Structure of heavy chain from strain 13
                                                                                                                                                                                                                                                        Trischmann T.M.
Submitted (APR-
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).
Enkarvota; Metazoa; Chordata;
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21-JUL-1986 (Rel. 01, Last
15-JUL-1999 (Rel. 38, Last
Ig gamma-2 chain C region.
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                                                                                                                            SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; PubMed=5538616;
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Hystricognathi; Caviidae; Cavia.
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RESULT 13
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ID GC1_MOUSE
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DT 21-JUL-1986
DT 21-JUL-1986
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Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea Biochemistry 10:26-31(1971).
Biochemistry 10:26-31(1971).
"YESPELIANEOUS: THIS CHAIN WAS ISOLA!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFIDE BONDS. MEDLINE-71058474;
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SM00407; IGC1; 2.
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EMBL; V00793; CAA24172.1;
EMBL; V00793; CAA24174.1;
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EMBL; V00793; CAA24175.1;
EMBL; V00795; CAA24176.1;
EMBL; V00795; GAA24176.1;
PIR; A02159; GIMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Immunoglobulin gamma 1 heavy cloned in a bacterial plasmid. Gene 9:87-97(1980).
                                                                                                                                                                    Pfam; PF00047; ig; 3. SMART; SM00407; IGc1;
                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The disulphide bridges of a mouse Biochem. J. 126:837-850(1972).
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MEDLINE=80202559;
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Honjo T., Obata M.,
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InterPro; IPR003006; I
InterPro; IPR003597; I
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GlycoSuiteDB; P01868;
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MEDLINE-81223894; PubMed=6787604;
Ollo R., Auffray C., Morchamps C., R
Ollo R., ar of mouse immunoglobulin
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"Structure of the constant and 3' untranslated
Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-2A chain C region, A allele.
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                                                                                                               "The complete nucleotide sequence of mouse is and evolution of heavy chain genes: further sequence-mediated domain transfer."; Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-81198976; PubMed-6262729;
Yamawaki-Kataoka Y., Miyata T., H
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Mammalia; Eutheria;
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MEDLINE-81076554; PubMed-6777755;
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PROSITE; PS00290; IG_MHC: 1
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MEDLINE-74175517; PubMed=4831970;
BOUTGOIS A., FOUGEGREAU M., ROCCA-Serra J.;

"Determination of the primary structure of a m
"munoglobulin:amino-acid sequence of the Fc for the evolution of immunoglobulin structure for the evolution of immunoglobulin structure for the growth of the structure for the evolution of immunoglobulin structure for the evolution 43:423-435(1974).
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"Determination of the primary structure of a mouse gamma immunoglobulin. Identification of the disulfide bridges.
Eur. J. Biochem. 30:452-462(1972).
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                                     ATPEWPGSRDKRTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSR
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SEQUENCE (MYELOMA PROTEIN NO.,)
MEDLINE=83289131; PubMed=6884994;
MEDLINE=83289131; PubMed=6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann J., Palm W., Hilschmann M.;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
Schmidt W.E., Lang W., Hilschmann N.;
Schmidt W.E., Lang W., Hilschmann N., Hilschmann N.;
Schmidt W.E., Lang W., Hilschmann N., Hilschmann N.;
Schmidt W.E., Lang W., Hilschmann N., Hilschmann N., Hillschmann N., Hillschmann N., Hillschmann N., Hilschmann N., Hillschmann N., Hill
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IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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Biochemistry 9:3188-3196(1970).
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"The rule of antibody structure. The primary structure monoclonal IgG1 immunoglobulin (myeloma protein Nie). chymotryptic peptides of the H-chain, alignment of the peptides and discussion of the complete structure."; Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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                                                  245 QVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 302
                                                                                                                                                                                                      71 VPSSS-LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK 129
                                                                                                                                                                                                                       17 STSGG-----TAALGCLVKDYFPEPVTVSW-NSGALTSGVHTFPAVLQSSGLYSLSSVVT 70
                                                                                                                                                                                                                                                                                  12 SCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGELASTQSELT 71
              KDEFICRAVHEAASPSQTVQRAVSVNPGK 320
: | | :||| | | :::|::||
                                                                 ---LACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQ 291
                                                                                                                                                                                                                                                                                                                                                               330 AA;
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                                                                                                                                                                                                                                                                                                          Gaps
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Search completed: July 15, 2003, 06:58:20 Job time: 10.9911 secs

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Maximum Match 100%
Listing first 45 summaries
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1707
1 FTPPTVKILQSSCDG
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1: /SIDS2/gcgdata/g
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution. ø

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1707	1707	1707	1707	1707	1707	1707	1707	1707	1707	Score	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Match	Query
428	428	367	331	325	325	324	323	323	323	Length DB	
23	23	9	21	16	16	16	23	23	23	DB	
AAM50940	AAU80283	AAP80291	AAB03642	AAR77241	AAR75225	AAR83559	AAU80286	AAU80285	AAU80284	ID	
Human IgE epsilon	Human IgE heavy ch	Interleukin-2/IgE	Human IgE heavy ch	Human IgE Fc chain	Human IgE Fc chain	Fc(epsilon) CH2'-C	Human IgE C2-C3-C4	Human IgE C2-C3-C4	Human IgE heavy ch	Description	

45	44	43	42	41	40	39	38	37	36	35 5	34	$\frac{\omega}{\omega}$	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
691.5	695	748	748	748	751	751	751	751	751	770	781	783	793	827	895.5	928.5	943	945	948.5	1013	1038	1038.5	1088	1158	1158	1663	1671	1677	1685	1693	1696	1696	1701	1707
40.5	•	٠	43.8	43.8	44.0	44.0	44.0	44.0	4.	5			•	•	52.5	•	•	•	•	59.3		•		67.8			•		•	•	•	99.4		100.0
313	130	432	343	343	421	341	332	332	332	345	341	313	340	341	312	417	424	424	426	190	209	342	201	222	218	428	330	315	325	493	441	336	325	428
21	16	23	23	23	23	21	23	23	23	21	21	21	21	21	21	18	23	23	17	16	10	21	16	22	16	14	23	16	16	տ	23	23	21	23
AAY79997	AAR85585	AAU80294 ·	AAU80296	AAU80295	AAU80300	AAB06206	AAU80299	AAU80298	AAU80297	AAB06207	AAB03644	AAY79996	AAB03643	AAB06208	AAY79995	AAW23067	AAM50104	AAM50103	AAR97753	AAR85584	AAP90010	AAB06205	æ	AAG65599	AAR85583	AAR42950	AAU80289	AAR85582	AAR83582	AAP40065	AAU80287	AAU80288	AAY79994	AAM47863
Mouse immunoglobul	ilon) CH2'-	Murine IgE heavy c	heavy	Murine IgE heavy c	Mouse IgE heavy ch	pepti		Murine IgE heavy c			Opossum IgE heavy		Rat IgE heavy chai		munoglobuli	IgE heavy	IgE heavy	IgE heavy	IgE. Cani	Fc(epsilon) CH2'-C	Residues 340-547 o	Immunogenic peptid	Fc(epsilon) CH2'-C	Amino acid sequenc	1101	IqE	Human IgE C2-C3-C4	Fc(epsilon) CH2'-C	H4	ce of human	heavy	_	iog Lobi	Human Ig-E heavy c

ALIGNMENTS

RESULT 1 AAU80284 30-JUL-2002 (first entry) AAU80284; AAU80284 standard; Protein; 323 AA.

IGE; allergy; human; antiallergic; immunosuppressive; antianaphylactic; antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IGE; vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis; heavy chain C domain.

Human IgE heavy chain C2-C3-C4 domains.

Homo sapiens.

Region Region Region Domain Domain Region Region Domain Key /note= "I /label= IgE heavy chain C3 domain 139..145 /note= "Epitope in DE loop"
196..206
/note= "Epitope in FG loop"
210..218 100..114 /note= "Epitope including C2C3 linker" 112..211 /note= Location/Qualifiers note= "IgE heavy chain C2 domain" "Epitope "Linker between domains C2 and in BC loop" C3

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Matches
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprises effecting simultaneous presentation of cytotoxic T hymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in an animal, which is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains used to create the
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lymphocyte epitope
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304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g immune response against autologous immunoglobulin E in an
by effecting simultaneous presentation of cytotoxic T
yte epitope an/or B-cell epitope derived from the immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autologous
                                                                                                                                                                                                                                                                                              FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                  HEAASPSQTVQRAVSVNPGK
                                                                                                                                   RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                            LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                                                                                     GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
    HEAASPSQTVQRAVSVNPGK
                                                                        NEMPEDISVOMLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                                                                                                                                                                        GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                          NEMPEDISYOWLHNEVOLPDARHSTTOPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                                                                                                             LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                    RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                        323 AA;
                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 105-106; 151pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Von Hoegen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000DK-0001326
2000US-232831P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Epitupc ...
212..215
/note= "Linker between domains C3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin E (IGE) in an animal. The meth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         __Epitope including C3C4 linker"
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                                                                                                                                                                                                                                                                                                                                                            0;
                                320
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Pred. No. 1.1e-129;
; Mismatches 0;
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Q 멍 Ş В Ωy В δÃ 밁 QY В δÃ

DЬ Ωy

64

Вb

4

QУ

121 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT

180

120 63

123

GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE

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Qy
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AAU80285
ID AAU8
                                                     Query Match
Best Local :
                                                                                                                                                presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains optimised for expression in a state of the present sequence.
                                                                                                                                                                                                                                                            comprises effecting simultaneous presentation of cytotoxic (CTL) epitope and/or B-cell epitope derived from IgE, and T epitope (TH epitope) which is foreign to the animal, by ant
                                                                                               Sequence
                                                                                                                                                                                                                                                                                                      This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E ({\tt IGE}) in an animal. The method
                                                                                                                                                                                                                                                                                                                                                                                    Inducing immune response against autologous immunoglobulin E in animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell apitope derived from the immunos
                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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15-SEP-2000;
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                                                             This invention relates to a novel method for inducing an immune response CC against autologous immunoglobulin E (IgE) in an animal. The method CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell CC epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes CC of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating CC autologous IgE in the animal. This method is useful in the prevention CC and treatment of allergic diseases such as anaphylaxis, allergic CC rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains optimised for expression in an E. Coli system, this sequence was used to create the epitopes of the
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constant heavy region; E.coli; glycosylation; antigenic; immunogenic;
histamine; anti-allergenic; vaccine; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fc(epsilon)-CH2'--CH4 protein-sequence
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The amino acid sequence of the Ec(epsilon) CH2'-CH4 fragment covering amino acids 226-547. The DNA sequence was isolated from a human myeloma 266BL cDNA library screened with a probe corresp. to the N-terminus of IgE. The region encoding amino acids 218-547 was cloned into the vector
                                                                                                                                                                                                            Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain - has epitope(s) not present in native IgE, also derived antibodies for treating or preventing allergies, inflammatory immune disease,
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                                                                                                                                   Page 32-33; 44pp; French
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                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324;
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RESULT 6
AAR77241
ID AAR7
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AC AAR7
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DT 10-N
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standard;

Protein;

325

10-NOV-1995 AAR77241; AAR77241

(first entry)

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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                allergy.
                                                                                                                                                                                                                                                                                                                            The sequence represents a mutant sequence of a human Ig chann framing acids. 224,54,74,74,161,615,615 receptor sites FC-epsilon RI and/or FC-epsilon FII BE receptor sites cells. The protein is useful in the study and treatmen
                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 6;
                                                                                                                                                                                                                                                                                                                                                                                                Mutated glycosylated polypeptide(s) contg. useful to study and treat allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gould HJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (THRE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-NOV-1993;
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 306
                                                                                   186
                                          246
                                                     241 NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                           181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                           1995-206936/27.
                                                                                                                                              121
                                                                                                                                                                    66
                                                                                                                                                                                                                                                      320;
                                                                                                                                                                           61 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                             σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 RES EXPL LTD.
CELLTECH THERAPEUTICS
                                                                                                                                                                                                                                                               Similarity
           HEAASPSQTVQRAVSVNPGK 320
                                                                                                                      LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
HEAASPSQTVQRAVSVNPGK
                                                                                                                                                                 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                   FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                         NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                         FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
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                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                           Score 1707; DB 16; Pred. No. 1.1e-129;
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Best Local S
Matches 320
                                                                                                                                                                                                                   The sequence represents the wild-type sequence of a human IgE-Fichain (amino acids 224-547) which is of sufficient length to bif re-epsilon RI and/or PC-epsilon FII IgE receptor sites on human cells. The sequence is preferably mutated (see AAR75225) to represent a protein encoding a protein where Cys225 is mutated, optionally together with Val224, Ser226 and Arg227. The protein is useful in the study and treatment of allergy.
                                                                                                                                                                                                                                                                              Disclosure; Page 35-36;
                                                                                                                                                                                                                                                                                           Mutated glycosylated polypeptide(s) contg. useful to study and treat allergy.
                                                                                                                                                                                                                                                                                                                  N-PSDB;
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                                                                                                                                                                                                                                                                                                                                       Gould
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
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                                                                                                                                                                                                       Sequence
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DB; AAQ91170.
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                                                                                                                                                                                Similarity
                                                                                                               NEMPEDIS VQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                           LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                            FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
             HEAASPSQTVQRAVSVNPGK
                                                              RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ-
                                                                                   LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
HEAASPSQTVQRAVSVNPGK
                           NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                       RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FC
                                                                                                                                                                                                                                                                                                                                       Owens RJ,
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                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                    EXPL LTD.
CH THERAPEUTICS
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172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 149
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiallergic
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                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                       Sutton BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                   "glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "glycosylation
                                                                                                                                                                                                                                                                            55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Asn394
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                                                                                                                                                                          0;
                                                                                                                                                                        Score 1707; DB 16;
Pred. No. 1.1e-129;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                     LTD.
             320
325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224-547) wild-type sequence.
                                                                                                                                                                                                                                                                                                                                      Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                         site"
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                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                IgE-Fc
to bind
human
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                                                                                                                                                                                                                                                                                                  IgE-Fc
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Query Match
Best Local S
Matches 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 50pp; English.
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22-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hellman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RESI-) RESISTENTIA PHARM AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mmunoglobulin
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                                                                                                  192
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; eczema; immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                        GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
HEAASPSQTVQRAVSVNPGK
                                                  NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                               GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                                                                                                        FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                                                                                                            FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides useful for preventing the harmful lin {\bf E} in mammals -
                                                                                                                                                                                                                                                                                                                                                                              Conservative
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99US-0401636.
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                                                                                                                                                                                                                                                                                                                                                                                                               331;
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RESULT 8
AAR80291
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                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                 This fusion protein has a low toxicity for allergy induced by IgE. It can be allergic dermatosis, atopic dermatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fused protein for allergy treatment - comprising interleukin-2 N\text{-}\text{terminal} residues, a linker and human immunoglobulin E Fc
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1988-149211/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-1987;
28-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-1987;
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                                 181
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                  RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                                                           FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60
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RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
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86JP-0281871.
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37..367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=IL-2 leader sequence 21..31
                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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Pred. No. 1.3
); Mismatches
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1.3e-129;
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                        Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglo
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15-SEP-2000;
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IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
vaccine; anaphylaxis, allergic rhinitis; asthma; atopic dermatitis;
heavy chain C domain.
                                                 (PHAR-) PHARMEXA AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human IgE heavy chain C1-C2-C3-C4 domains
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2002-383033/41.
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2000US-232831P
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                      Hoegen
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321..422
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317..3
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244..2
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                                                                                                                                                                                        "IgE heavy
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immunoglobulin

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RESULT 10
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AC AAM50
AC AAM50
AC Human
XX IJE;
KW IJE;
KW UITLIC
KW ANTII
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Best Local S
Matches 320
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                                                                                                                                                            urticaria; anaphyl
antianaphylactic;
antiinflammatory;
                                                                                                                                                                                                                                                                                                                               AAM50940
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                                                                                                                                                                                                                                       Human IgE epsilon chain constant region
   WO200209751-A2
                                              Domain
                                                                          Domain
                                                                                                                     Homo sapiens
                                                                                                                                                 vaccine;
                                                                                                                                                                                                                                                                      15-MAY-2002
                                                                                                                                                              immunoglobulin E; antibody; human; allergy; asthma; eczema;
caria; anaphylactic shock; allergic rhinitis; conjunctivitis;
anaphylactic; immunosuppressive; antiallergic; antiathamatic;
inflammatory; dermatological; vasotropic; ophthalmological;
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                                                                                                                                                                                                                                                                                                                                 standard;
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                                                                                                                                                 therapy.
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                             /label= CH1
313..428
/label= CH4
                                                                                      Location/Qualifiers
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Pred. No. 1.5e-1
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Constant region. The invention is based on the discovery that a constant region. The invention is based on the discovery that a constant region. The invention is based on the discovery that a constant region. The invention of a carrier, can be used to induce in a mammal the production of carrier, can be used to induce in a mammal the production of compositions are provided for inducing self-specific anti-IgE compositions are provided for inducing self-specific anti-IgE coupled to polypeptides contain carriers foreign to the immunised mammal coupled to polypeptides containing fragments of the IgE molecule, coupled to polypeptides containing fragments of the IgE molecule, coupled to polypeptides containing fragments of the IgE molecule, coupled to polypeptides containing fragments of the IgE molecule, coupled to polypeptides have at least 95% identity to amino acids 1-110, 105, 5-105 or 5-95 of the present sequence, while CH4 polypeptides have at least 95% identity to amino acids containing and polypeptide in the mammal's serum. Alternatively, a polynucleotide encoding a fusion comprising the coarrier and IgE-derived polypeptide is compositions and polynucleotides are used to indicate the polynucleotides are 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition for treating immunoglobulin (Ig) E-mediated disorder such as anaphylactic shock, allergic rhinitis and conjunctivitis, comprises a polypeptide that includes CH1 and/or CH4 domains of IgE molecule coupled to a carrier
                                                  an allergen such as fur, dust or freezema or urticaria (all claimed).
                                                                               inhibit or treat IgE-mediated disorders such as anaphylactic shock, allergic rhinitis or conjunctivitis, an allergic reaction an allergen such as fur, dust or food, an asthmatic reaction,
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                                                                                                   229
                                                                                                                       121
                                                                                                                                           169
                                                                                                                                                                                  109
                                                                                                                                                                                                                          320;
                                                                                                                                                              61
                                                                                                                                                                                                                         Similarity 100
20; Conservative
                                                                                                                                         HEAASPSQTVQRAVSVNPGK
                              NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                     RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                   LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                             LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                   NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                          RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                        Score 1707; DB 23;
Pred. No. 1.5e-129;
Mismatches 0;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                         Gaps
                                      300
                                                                                                                       180
                                                                                                                                                              120
                                                                                                                                                                                  168
                                                                             240
                                                                                                 288
                                                                                                                                           228
                                                          348
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409

HEAASPSQTVQRAVSVNPGK 428

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80 A

Qy Db

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                                                                                                                                                  reducing infection by human rhinovirus (HRV) and hence the initiation or compared of the common cold by HRV. The immunoadhesin binds to HRV and reduces its infectivity, competing with cell surface ICAM-1 for binding sites, interfering with virus entry or uncoating and directing premature release of viral RNA and formation of empty capsids. Expression of the immunoadhesin in plants would be tetrameric, rather than dimeric.

Immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectiveness of the immunoadhesin. Association of secretory component and immunoglobulin J chain increases the stability of the immunoadhesin in the mucosal environment. Production is significantly less expensive in plants than in animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a human immunoglobulin protein sequence, useful to
                                                                                           Query Match
Best Local
                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin heavy chain; and (b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J chain and secretory component in association -
                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       chimeric ICAM-1 molecule. The immunoadhesin has plant-specific glycosylation and virucide activity. The immunoadhesin is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an immunoadhesin comprising:

(a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising rhinovirus receptor protein linked to at least a portion of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Ig-E heavy chain constant region amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM47863 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PLAN-) PLANET BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-2000; 2000US-200298P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-APR-2001; 2001WO-US13932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       numan rhinovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-041481/05
DB; ABA05278.
     109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoadhesin;
                                                                                             Similarity
FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60
                                                                                                                                                  428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 7; 138pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wycoff KL
                                                                           Conservative
                                                                                                                                                  AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin heavy chain; J
                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intercellular adhesion molecule; ICAM-1;
unoglobulin heavy chain; J chain; HRV; common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                           0;
                                                                                          Score 1707; DB Pred. No. 1.5e-1
                                                                         Mismatches
                                                                         Indels
                                                                                                         Length
                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cold;
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and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe
                                                                                                                                                                                                                                                                                                                                                                 The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenic; immuno
antibody; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunoglobulin E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNBI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY79994 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin E; IgE; epsilon heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigenic peptide from the CH3 domain of immunoglobulin E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Page 66-68; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEMPEDIS VQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEAASPSQTVQRAVSVNPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Walfield AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in E; IgE; epsilon heavy chain; antigenic; antigen;
immunostimulatory; carrier protein; helper T cell er
lergy; allergic disease; immunisation; anti-allergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0100287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US13959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  against allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320
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6
AAY80084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid
                                                                                                                                                                                                             IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic; antiasthmatic; dermatcological; antiinflammatory; immunoglobulin E; IgE; vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis; heavy chain C domain; MIGIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Domain
                                                                                                                                                                                                                                                                     30-JUL-2002
                                                                                                                                                                                                                                                                                                     AAU80288
                 Domain
                                Region
                                                                Region
                                                                              Region
                                                                                              Region
                                                                                                               Domain
                                                                                                                               Region
                                                                                                                                              Region
                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                     Human IgE heavy chain C2-C3-C4 domains with MIGIS fragment
                                                                                                                                                               Domain
                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences
                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                            246
                                                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                            186
                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                           126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein; 336
                                                                                                                                                                                                                                                                                                                                                    HEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                            NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWQEKDEFICRAV
                                                                                                                                                                                                                                                                                                                                                                                     NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                                                                                                                             HEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used
                                                                                                                /note=
112..2
                                                                                                                               /note= "
104..111
                /note=
216..31
                                /note=
212..2
                                                /note=
210..21
                                                                /note=
196..20
                                                                                               /note= "IgE heavy chain C3
139..145
                                                                                       /note=
                                                                                                                                              /note= "IgE heavy chain C2 domain"
100..114
                                                                                                                                                                      Location/Qualifiers
                                                                                167..175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in
                                                                ..206
                                .215
                                                .218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.6%;
                                                                                                               . 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                        "Linker between domains C3 andC4"
                                                       "Epitope
                                                                     "Epitope
                                                                                     "Epitope in
                                                                                                                      "Linker domain between C2 and C3 region"
                                                                                                                                      "Epitope including C2C3 linker"
        "IgE heavy chain C4 domain"
                                       "Epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1701;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                             325
                                                                                                                                                                                                                                                                                                                                                             320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                     ĀĀ
                                       including C3C4 linker"
                                                       in
                                                                       'n
                                                       FG
                                                                       DE loop"
                                                                                       BC loop"
                                                       loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .3e-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DВ
                                                                                                        domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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15-SEP-2000;
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               HEAASPSQTVQRAVSVNP
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RESULT

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This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen
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15-SEP-2000;
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presenting
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2000US-232831P
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dermatological; anti
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427..4:
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318..3
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antiinflammatory; immunoglobulin E; IgE;
rhinitis; asthma; atopic dermatitis;
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                                         Polypeptide
from host tr
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                                            recombinant
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                                                                  of human
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Pred. No. 1.2e-128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunological
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                                                                immunoglobulin
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Disclosure;

Fig

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English

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 밁
                      Qy
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Best Local Similarity 99.4%;
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding IgE H-chain and frags. is claimed (AAN40062). Transformant contg. the DNA is also new, esp. Escherichia coli IFO-14284, -5 and -6. The transformant may be grown to produce a polypeptide of immunological or biological activity equivalent to that of the human IgE H chain. AAN40062 or frags. is pref. linked at a site downstream from a promoter, e.g. rec A promoter (see AAN40064).
414
                                                              241 NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 300
                                                                                                    354
                                                                                                                             181
                                                                                                                                                   174
                                                                                                                                                                                                                                                       RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                                                  NFMPEDISVQWLHNEVQLPHARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICPAV 473
                                                                                                  RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                              493 AA;
                                                                                                                                                                                                                                                                                                          Score 1693; DB 5;
Pred. No. 2.5e-128;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                Length 493;
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Search completed: July 15, 2003, 06:57:40 Job time: 39.6806 secs

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                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB
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430.5
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seg length: 2000000000
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1707
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1: sp_archea:
  26.3
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sp_phage:*
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sp_bacteriap:*
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                                                                                                                                                                                                                                                                                                        sp_unclassified:*
                                                                                                                                                                                Length
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1833.165 Million cell updates/sec
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                                                                                                               Q95M34
Q8VCX7
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Q9BSZ1
Q99LC4
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Q96BB9
Q9BU10
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Q9RWUX4
Q96EY0
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Q96GA6
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         Q8wuk1 |
Q96ga6 |
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193	279	296	296	296	296	296	296	297	299.5	301.5	303.5	303.5	306	306	306	323.5	331.5	3 3 3	334.5	334.5	334.5	347	357	363.5	389	389	389.5	399
11.3	16.3	17.3	17.3	17.3	17.3	17.3	17.3	17.4	17.5	17.7	17.8	17.8	17.9	•	17.9		٠	19.5 .	•	•	•	•	•		•	•	22.8	•
573	684	489	488	484	482	481	481	480	479	.426	487	486	484	481	479	500	496	497	496	494	384	416	701	473	474	473	473	471
4	13	11	11	11	11	11	11	11	11	片	11	1	11	11	11	4	4	4	4	4	4	4	4	11	11	11	4	4
Q8WU38	Q90544	Q8VCX4	Q91WR1	Q8VEA0	Q91X92	Q91WT1	Q91WT3	Q91XE1	Q91WP5	Q9DCD9	Q99KA4	Q91Z07	Q99LA6	Q8VCV5	Q99M22	Q9BRV0	Q96DK0	Q8WY24	Q96KX8	Q96K68	Q9UP60	Q9NPP6	Q96PQ8	Q9D8L4	Q8R3H6	Q91Z05	Q8TC63	Q8TC77
-	Q90544 ginglymosto	Q8vcx4 mus musculu	Q91wr1 mus musculu	Q8vea0 mus musculu	Q91x92 mus musculu	mus	Q91wt3 mus musculu	Q91xel mus musculu	Q91wp5 mus musculu	Bus	mus	mus	mus	mus	2 mus	homo	Q96dk0 homo sapien	homo	homo	homo	homo	homo	Q96pq8 homo sapien	mus	Buns	5 mus	Q8tc63 homo sapién	Q8tc77 homo sapien

ALIGNMENTS

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RESULT 1
Q95M34
                                                           Query Match
Best Local Sim
Matches 106;
                                                                                                                                Wagner B., Overesch G., Sheoran A., Holmes M., Richards C., Leibold W., Radbruch A.; Leibold W., Radbruch A.; "Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."; Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
                                                                                                                                                                                                                                                                                                                                   Equus caballus (Horse).
Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation update)
Immunogobulin gamma 1 heavy chain constant region
                                                                                    Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=98383416; PubMed=9717671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q95M34;
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                                                                                                                                                                                                                                                                      Submitted (DEC-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                            SEQUENCE
                                                                                                                  InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9796;
                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                             IGHC1.
               Similarity
                                                           337 AA;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                           37438 MW; A60BF2B01DEFD1F6 CRC64;
 26.3%; Score 448.5; DB 6; 31.3%; Pred. No. 1e-32; tive 62; Mismatches 146;
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                                                                                                                                                                                                                                                                        databases
                             Length 337;
 Indels
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2 TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEG

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RESULT
OBVCX7
ID Q8VCX7
ID Q8
AC Q8
AC Q8
DT Q1
DT Q1
OC F Q8

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Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; 19; 5.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 4.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 67.9 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=SALIVARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-2001) to the EMBL; BC018315; AAH18315.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003599;
InterPro; IPR003597;
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                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                          PTVKILQSSCDG-GGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                    SVCVEDWNNRKEFVCTVTHRDLPSPQKKFISKPNEVHKHPPAVYLLPPAREQLNLRESAT
                                                                                                                                                                                  GSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLTFLKNVSSTCAASPSTDILTFTIPP
                                                              PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP--EWPGSRDKRT
                                                                                                   SFADIFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPNGTFSAKGVA
                                                                                                                                                                                                                                                              PNVNVFVPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEEQFNSTYRVVSVLRIQHQDWLSGKEFKCKVNNQALPQPIERTITKTKGRSQEPQVYVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFYSLSSMYTVPASTWTSE-TYICNVVHAASNFKVDKRIEPIPDNHQKVCDMSKCPKCPA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSVDRNRWQQGTTFTCGVMHEALHNHYT-QKNVSKNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAPKVFALAPGC -- GTTSDSTVALGCLVSGYFPEPVKVSW-NSGSLTSGVHTFPSVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APHPDELSKSKYSYTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQQDSDGSYFLYSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRK
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig_c1.
Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                              25.2%;
                                                                                                                                                                                                                                                                                                                                               56;
                                                                                                                                                                                                                                                                                                                                           Score 430.5; DE Pred. No. 1e-30; 6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Sciurognathi; Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽
                                                                                                                                                                                                                                                                                                                                                                                  DB 11;
                                                                                                                                                                                                                                                                                                                                             149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -DSTKKCADSN--PR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                     613;
                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus.
                                                                                                                                                                                                                                                                                                                                             Gaps
                    487
                                                            234
                                                                                                                                                                                368
                                                                                                                                                                                                                                                              308
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Q9BSZ1
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Q8R3V9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                         Q9BSZ1;
01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                            Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                          Q9BSZ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9R3V9;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                    Hypothetical 41.3 kDa protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAR-2002) to the
EMBL; BC024405; AAH24405.1;
TISSUE=LYMPH;
                  SEQUENCE FROM N.A.
                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical 52.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8R3V9
                                                                                                                                                                                                                                                                               4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Similarity
97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPPSVYPLAPG--SAAQTNSMVTLGCLVKGYFPEPVTVTW--NSGSLSSGVHTFPAVLQS
                                                                                                                                                                                                                                                                                                                                           GNTFTCSVLHEGLHNHHT-EKSLSHSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLYTLSSSVTVPSSTWPS-QTVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVF
                                                                                                                                                                                                                                                                                                                                                                                KDEFICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                                                                                                                                                                                                                                                      KVSLTCMITDFFPEDITVEWQWN--GQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTKPREEQFNSTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELASTQSELTLSQKHWLSDRTYTCQVTYQGHTF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGS-GF-FVFSRLEVTRAEWEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETYTCVVGHEAL-PHLVTERTV 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFICRAVHEAASPSQTVQRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTHSILTVTEEEWNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al protein.
469 AA; 5
                                                                                                                                                         (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                             Chordata;
                                                                            Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51976 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 414; DB
Pred. No. 2.3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                            Craniata; V
Catarrhini;
                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    534793F155D05457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                          375
                                                                                                                                                                                                                                                                                                                                             469
                                                                                               Vertebrata;
                                                                            Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154;
                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - EDSTKKCADSNPRGVSAY
                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
Murinae; Mus
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469; 18;

Gaps

231

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RESULT
Q99LC4
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Best Local S
Matches 94
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InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (MAR-2001) t
EMBL; BC004476; AAH044
HSSP; P01857; 1FC1.
                    Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 2.
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like
                                                                                                                                                                                                                                                                                                                                                                                  099LC4 PRELIMINARY: PRT; 4
099LC4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seque
01-JUN-2002 (TrEMBLrel. 21, Last annot
Similar to RIKEN CDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                      Jimir

IGH-4.

Mus musculus (Mouse).

Mus musculus (Mouse).

Metazoa; Chordata;

Meria; Rodentia;
                                                                                                                    InterPro;
InterPro;
                                                                                                                                                                                  EMBL; BC003435; AAI
HSSP; P01842; 7FAB
MGD; MGI:96446; Igh
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 375 AA; 4
                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                   Strausberg
                                                                                                      InterPro;
                                                                                                                                                     InterPro;
                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                              *2; 7FA...
*2; 7FA...
*36446; Igh-4.

*36446; Igh-4.
*36446; Igh-4.
*3646; Igh-4.
*364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LA----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LACLIONEMPEDISVOWLHNEVQLPDARHSTTQPR-KTKGSG-FFVFSRLEVTRAEWEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETYTCVVAHEAL - PNRVTERTVDKSTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                                                                                                                                                                                    (FEB-2001) to the 
03435; AAH03435.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
; iG; 2.
7; iGc1; 2
1Gv; 1.
iG_like; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH04476.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 413; DB 4;
Pred. No. 2.1e-29;
3; Mismatches 159
                                                                                                                                                                                                                                                                                                                  Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B1A0A0998F473619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357
                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                      Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                      Murinae;
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                                                                                                                                                                                                                                                                                                                      Mus
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Q9BQB8
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SQ
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                    Query Match
Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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SEQUENCE
                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
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InterFig. 19; 5.

Pfam; PF00047; 1G; 2.

SMART; SM00409; IGc1; 4.

SMART; SM00406; IGc1; 4.

SMART; SM00410; IG_11ke; 1.

SMART; SM00410; IG_MHC; UNKNOWN_3.

PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JAN-2001) to the
Submit econol180; AAH06180.1;
EMBL; BC001872; AAH01872.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9BQB8 PRELIMINARY; PRT; 597 AA.
Q9BQB8;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Unknown (protein for MGC:1905) (protein for MGC:1228).
                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R. Submitted (API
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                             TISSUE=LYMPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          HSSP; P01825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00290; 1
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELASTQSELTLSQKHWLSDRTYTCQVTYQGHTF-----EDSTKKCADSNPRGVSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPPSVYPLAPG---SAAQTNSMVTLGCLVKGYFPEPVTVTW--NSGSLSSGVHTFPAVLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLYTLSSSVTVPSSTWPSE-TVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDEFICRAVHEAASPSQTVQRAVSVNPGK
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                                                                                                                                                                                                     IPR003006;
                                                                                                                                                                                                                                       IPR003597;
                                                                                                                                                                                                                                                        IPR003599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG_MHC; UNKNOWN_1.
; 51007 MW; EAA674C6BBC30783
                                                                                                                                                                                  Ig_cl.
Ig_like.
Ig_MHC.
Ig_v.
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29.2%;
               24.2%;
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Score 413; DB
Pred. No. 3.9e
53; Mismatches
                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 413; DB 11;
Pred. No. 2.8e-29;
1; Mismatches 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                   2DAFAD50A6375851 CRC64;
e 413; DB 4; I
. No. 3.9e-29;
ismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae;
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                                                                                                                                                                                                                                                                                                                          databases
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                               Length 597;
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Conservative

63;

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Best Local S
Matches 94
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Submitted (OCT 2001) to the EN Submitted (OCT 2001) to the EN EMBL; BC015760; AAH15760.1;
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 5.
PROSITE; PS00290; IG_MHC; UNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC 2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Hypothetical 65.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein SEQUENCE 597 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          096вв9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-B-CELL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q96вв9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
        493
                                                                                                                                   177
                                                                                                                                                                               374
                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                    314
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                                                                                                                                                                                                                                                                                                                                                    254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254
                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                         94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
    ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                     LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVFSRLEVTRAEWEQK
                                                                                    PPTVKILQSSCDGGGHFPPTTQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE 62
                                                                                                                                                                         SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                                                                                                                                                 SPEDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                   LA----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP 116
                                                                                                                                                                                                                                                                                                                                              PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                                                                                                                             ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LACLIQNEMPEDISYQWLHNEYQLPDARHSTTQPR-KTKGSG-FFVFSRLEVTRAEWEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETYTCVVAHEAL - PNRVTERTVDKSTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LA-----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP 116
: | | | | : : | | :| :| | ::: | : : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-ATPEWPGSRDKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG_MHC; UNKNOWN_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65039 MW; 4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 413; DB 4;
Pred. No. 3.9e-29;
3; Mismatches 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                313
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RESULT
Q9R1A4
ID Q9
AC Q9
DT 01
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Q9BU10
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPRO03606; Ig_MHC.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 4.
SMART; SM00401; IGc1; 4.
SMART; SM00401; IGc1; 4.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
Q9R1A4;
Q9R1A4;
Q1-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00
Hypothetical
SEQUENCE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ol-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequol-DEC-2001 (TrEMBLrel. 19, Last ann Hypothetical 65.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC002963;
HSSP; P01825; 7E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (FEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BU10;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BU10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=LYMPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003597;
                                                                                    9
                                                                                                                                                   553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                      LACLIQUEMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVFSRLEVTRAEWEQK
                                                                                                                                                                                           DEFICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                ETYTCVVAHEAL - PNRVTERTVDKSTGK
                                                                                                                                                                                                                                                                                                                     SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LA-----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE 62
                                                                                                                                                                                                                                                                                                                                                             PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-ATPEWPGSRDKRT
                                                                                                                                                                                                                                                                                                                                                                                                        SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL 176
                                                                                                                                                                                                                                   ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETYTCVVAHEAL - PNRVTERTVDKSTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFICRAVHEAASPSQTVQRAVSVNPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 protein
597 AA;
(TrEMBLrel.
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                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65274 MW; 2DAFA8FB7E055851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig.
Ig_c1.
Ig_like.
Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.2%; Score 413; DB 4; 28.7%; Pred. No. 3.9e-29;
13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63;
Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
annotation update)
                                          437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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313

373

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Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wilde K.G., Yu.X., Ekramoddoullah A.K.M., Misra S.;

"Cloning of cDNAs encoding for anti-white pine blister rust
antibody (Mab 7, its light and heavy chains) and construct:
single chain antibody (scFV).";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF152372; AAD40243.1; -

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
R HSSP; PD1842; 7ABB
R MGD; MGI:96446; Igh-4.
InterPro; IPR003500; Ig_MHC.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR00359; Ig_WHC.
R InterPro; IPR00359; Ig_WHC.
R InterPro; IPR00359; Ig_WHC.
R InterPro; IPR00359; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (
01-JUN-2002 (
Gammal heavy
                                                                                                   OSWUX4, PRELIMINARY; PRT; 588 AA.
OSWUX4;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
NON_TER
NON_TER
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IGH-4.
Mus musculus (Mouse).
Mus musculus (Mouse).
Thervota; Metazoa; Chordata; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 2.
  TISSUE-LYMPH;
              SEQUENCE FROM
                                      NCBI_TaxID=9606;
                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                               Hypothetical 64.4 kDa protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  410
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97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               TPPSVYPLAPG--SAAQTNSMVTLGCLVKGYFPEPVTVTW--NSGSLSSGVHTFPAVLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00290; IG_MHC; UNKNOWN_1
                                                                                                                                                                                                                                                         KDEFICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                                                                                                                                                                                                                                           SVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD
                                                                                                                                                                                                                                                                                                                                                        VTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLYTLSSSVTVPSSTWPSE-TVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELASTQSELTLSQKHWLSDRTYTCQVTYQGHTF-----EDSTKKCADSNPRGVSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEG
                                                                                                                                                                                                                                 GNTFTCSVLHEGLHNHHT-EKNLSHSPGK
                                                                                                                                                                                                                                                                                KRTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQ
                                                                                                                                                                                                                                                                                                                                                                                              IFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                437
437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 21, Last annotation updat y chain of Mab7 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                437
                                                     Primates;
                                                                  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48142 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.1%; Score 411; DB 11; 29.5%; Pred. No. 3.9e-29; Live 59; Mismatches 155
                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5C3A7BB3EE7D697C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K.M., Misra S.;
white pine blister rust
chains) and construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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RESULT 11
Q96EY0
ID Q96EY
AC Q96EY
AC Q96EY
AC Q96EY
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT Unknn
OS Homo
OC Eukal
OC Mamma
OX NCBL
A
RN (1)
RN (1)
RR FEMBLI
RN Intel
DR Intel
DR Intel
DR Intel
DR Intel
DR SMART
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Best Local S
Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_wHC.
InterPro; IPR003596; Ig_w.
Pfam; PF00047; Ig; 5.
SMART; SM00409; IG; 2.
SMART; SM00409; IGc1; 4.
SMART; SM00406; IGv; 1.
PR0017E; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                               VI-MAR-2002 (TrEMBLrel. 20, Last annotation Unknown (protein for MGC:20337).
                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2001) to the EMBL; BC019235; AAH19235.1;
                                                                                         Pfam; PF00047; ig; 5.
SMART; SM00408; IGc2; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_3
                                                                                                                                   Submitted (JUL-2001) to the EMBL; BC011857; AAH11857.1; InterPro; IPR003598; Ig_c2. InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE-B-CELL;
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein SEQUENCE 588 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R
                                                              SEQUENCE
                                                                                                                                                                                             Strausberg R.;
                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                               Q96EY0;
                                                                                                                                                                                                                                                                                                                                                                                                Q96EY0
                                                                            mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293
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   l Similarity
92; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LA----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-ATPEWPGSRDKRT
: || || : | || || : : : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETYTCVVAHEAL - PNRVTERTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFICRAVHEAASPSQTVQRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVFSRLEVTRAEWEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                              613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                              AA.
                                                                              domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64438 MW;
                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; I Primates; Catarrhini; Hominidae;
                                                              67273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.7%;
                 23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
               Score 404; D
                                                                                                                                                                                                                                                                                                                                                Last
                                                                                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 404; DB 4;
Pred. No. 2.5e-28;
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                                                              31214203FB8421E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                 sequence update)
1.7e-28;
nes 156;
                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                  databases
                             Length 613;
                                                              CRC64;
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                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Conservative

62;

Mismatches

Indels

12;

Gaps

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RESULT 12
08WUK1
ID 08WUK
AC 08WUK
AC 08WUK
DT 01-MA
DT 01-JU
DE HYPOOL
OS HOMO
OC EUKBAT
OC MARIMBA
OT 01-WI
RA SEQUE
RC TISSU
RA STRAU
RL SUBMI
INTER
DR SMART
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Best Local S
Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 5.
SMART; SM00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 67.3 kDa protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. SEQUENCE 613 AA; 67296 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2001) to the EMBL/GenBank/DDBJ EMBL; BC020240; AAH20240.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8WUK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8WUK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003599;
InterPro; IPR003597;
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     177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00407; IGc1; 4.
SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                             ch 23.7%;
l Similarity 28.6%;
92; Conservative 6
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                                                                                                                                                                                              LA-----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP
                                                                                                                                                                                                                                                      PRVSVEVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-ATPEWPGSRDKRT
                                               SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                            SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                      ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                        PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETYTCVVAHEAL - PNRVTERTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFICRAVHEAASPSQTVQRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-ATPEWPGSRDKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LA-----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig.
Ig_c1
                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                                                                          Score 404; DB 4; I
Pred. No. 2.7e-28;
2; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60C7F5950671E315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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234
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                                               RESULT 14
Q96AA6
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Q96A0

ID GA6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 92
Q96AA6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissue=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                       PRELIMINARY;
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Q96GA6 PRELIMINARY; PRT; 614 AA. Q96GA6; O1-DEC-2001 (TrEMBLrel. 19, Created) O1-DEC-2001 (TrEMBLrel. 19, Last sequence update) O1-MAR-2002 (TrEMBLrel. 20, Last annotation update) Unknown (protein for MGC:15420).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003006; Ig_MHC.

Pfam; PF00047; 19; 5.

SMART; SM00408; IGC2; 2.

PROSITE; PS00041; HTH_ARAC_FAMILY_1;

PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; BC009851; AAH09851.1; -. InterPro; IPR000005; HTHArac. InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Emmunoglobulin domain.
SEQUENCE 614 AA; 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Similarity
| 92; Conserv
                                                                                                                                               LACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVFSRLEVTRAEWEQK
                                                                                                                                                                                                                                                                                                                                                                                             ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                           LA-----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                             DEFICRAVHEAASPSQTVQRAV
                                                                                               ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                                                                                                                                                               SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                             PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-ATPEWPGSRDKRT
                                                                                                                                                                                                                                                                                               SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVFSRLEVTRAEWEQK 292
ETYTCVVAHEAL-PNRVTERTV
                                                                                                                                                                                                                                                                                                                                             SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETYTCVVAHEAL - PNRVTERTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFICRAVHEAASPSQTVQRAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67921 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.7%; Score 404; DB 4; Length 614; 28.6%; Pred. No. 2.7e-28; Live 62; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55EF536E77AA9BBB CRC64;
                                                  314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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PRT;

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Q99L31
ID Q99L3
ID Q99L3
D99L3
AC Q99L3
D7 01-U0
D7 01-U0
D7 01-U0
D7 01-U1
D8 Mus n
OC Eukar
OC Musman
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Best Local (
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Q99L31;
Q99L31;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
Mus musculus (Mouse).

Chardata Craniata: Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017356; AAH17356.1; -.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003065; Ig_MHC.
Pfam; PF00047; ig; 5.
SMART; SM00408; IGC2; 1.
PROSITE; PS00290; IG_MC; UNKNOWN_3.
Hypothetical protein; Immunoglobulin domain.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 67.8 kDa protein.
                                                        InterPro;
InterPro;
                                                                                                             Strausberg R.;
Submitted (FEB-2001)
EMBL; BC003878; AAH03
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-LYMPH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                 InterPro;
                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 PPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-ATPEWPGSRDKRT
: || || : | |: | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LA----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCADSNPRGVSAYLSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETYTCVVAHEAL - PNRVTERTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFICRAVHEAASPSQTVQRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVFSRLEVTRAEWEQK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE
                              IPR003599;
IPR003597;
IPR003600;
        IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                         2001) to the AAH03878.1;
Ig.
Ig_c1.
Ig_like.
Ig_MHC.
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A Pfam; PF00047; 1g; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00410; IG_Like; 1.

DR SMART; SM00410; IG_MHC; UNKNOWN_1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

PROSITE; PS
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Search completed: July 15, Job time : 36.9679 secs 2003, 07:01:48

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/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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sequence 3, Appii	ر د	Secuence 3 Appli	27,	Sequence 34, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 33, Appl	<u>5</u>	۳	11,			Sequence 2, Appli	Sequence 14, Appl	-	28,	Sequence 9, Appli	Sequence 8, Appli	ω Α	Sequence 2, Appli	Sequence 6, Appli	14,	Sequence 10, Appl	-	12,	Sequence 26, Appl

ALIGNMENTS

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Publication No. COLD REPORT ON STANDARD OF SEQ ID NOS: 177

Publicant: Saxon, Andrew APPLICANT: Zhang, Ke APPLICANT: Zhang, Ke APPLICANT: Zhang, Ke APPLICANT: Zhu, Daocheng TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES FILE REFERENCE: UC67.002A

CURRENT APPLICATION NUMBER: US/09/847,208

CURRENT FILING DATE: 2001-05-01
                                                                                                                                                                                                                                                                                                                                                                                                 US-09-847-208-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6
LENGTH: 320
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                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                     ; NAME/KEY: MISC_FEATURE : LOCATION: (196)..(206) ; OTHER INFORMATION: Epitope US-09-949-375A-2
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CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 323
                                                                 Query Match
Best Local
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                                                     Matches
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TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 323
TYPE: PRT
ORGANISM: homo sapiens
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                                                                                                                                                                 NAME/KEY: MISC_FEATURE LOCATION: (167)...(175) OTHER INFORMATION: Epit
                                                                                                                                                                                                                    NAME/KEY: MISC_FEATURE LOCATION: (139)..(145) OTHER INFORMATION: Epi
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OTHER INFORMATION: Epitope
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OTHER INFORMATION: Linker
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RESULT 4
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; OTHER INFORMATION: Artificial amino
US-09-949-375A-4
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US-09-949-375A-4
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LENGTH: 323
TYPE: PRT
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TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
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Pred. No. 8.4e-122;
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Sequence 1, Application US/1017664
Publication No. US20030031663A1
GENERAL INFORMATION:
APPLICANT: Heliman, Lars T.
ITTLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION UMBER: US/10/176,664
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR FILING DATE: 1990-9-22
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
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                                     ; OTHER INFORMATION: Synthetically US-10-176-664-1
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Best Local S
Matches 320
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APPLICANT: KLYSNER, Steen et al.
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                              SOFTWARE: FastSEQ for
SEQ ID NO 1
LENGTH: 331
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Query Match
Best Local Similarity
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                      TYPE: PRT ORGANISM: Artificial
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Pred. No. 8.4e-122;
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; OTHER INFORMATION: US-10-207-655-329
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US-10-207-655-329
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APPLICANT: Hayden-Ledbetter, Martha S.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT FILING DOMABER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 329
LEMGTH: 331
TYPE: PRT
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Best Local Similarity
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                                  NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                    NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
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                                                                                                                                                             Sequence 5, Application US/09847208
Publication No. US20030082190A1
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5
LENGTH: 427
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Matches
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                                                              APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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SEQ ID NO 1
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CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hellman, Lars T.

TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetically generated 09-401-636-1
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ORGANISM: Artificial Sequence
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hes 320;
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US-10-047-542-60
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                                                                                                                                                                                                                                         Matches
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Best Local :
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Best Local
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CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR
TITLE OF INVENTION: AND BACTERIAL DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 030905.0004.CIP1
                                                                                                                                                                                                                                                                                                                                       LENGTH: 42
TYPE: PRT
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hes 320;
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181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
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                                                                                                                    61 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
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Similarity 100.0%;
                                                   LFTRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                   GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
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                                 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
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Pred. No. 1.2e-121;
; Mismatches 0;
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RESULT 10
US-09-949-375A-1
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TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09949375A Patent No. US20020172673A1
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FEATURE:
NAME/KEY: DOMAIN
LOCATION: (113)..(208)
OTHER INFORMATION: Human
-09-949-375A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 42
TYPE: PRT
                                                                                                                                                                                             LOCATION: (317)..(320)
OTHER INFORMATION: Linker
                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE LOCATION: (301)...(311) OTHER INFORMATION: EPit
                                                                                                                                                                                                                                                                                                               NAME/KEY: MISC_FEATURE
LOCATION: (272)..(280)
OTHER INFORMATION: Epitope
                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: DOMAIN LOCATION: (11)...(116) OTHER INFORMATION: Human
                                                                                                                                 LOCATION: (321)..(422)
OTHER INFORMATION: Hum
                                                                                                                                                   NAME/KEY: DOMAIN LOCATION: (321).
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                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (244)..(251)
OTHER INFORMATION: Epitope
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OTHER INFORMATION: Linker
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                                                                           OTHER INFORMATION:
                                                                                          NAME/KEY: DOMAIN LOCATION: (217).
                                                                                                                     FEATURE:
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US-09-916-230-1
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APPLICANT: Bachmann, Martin F.
APPLICANT: Renner, Wolfgang A.
TITLE OF INVENTION: Compositions i
TITLE OF INVENTION: Antibodies at
FILE REFERENCE: 1700.0140001
                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US Patent No. US20020146422A1
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Best Local
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CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US 60/221,841
PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 428
TYPE: PRT
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                                                                                                                                                                 GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD 120
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NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                              RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
                                                                                       LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
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                             RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
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Pred. No. 1.2e-121;
); Mismatches 0;
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1 FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                       NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 300
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Antibodies and Uses for Inducing Self-Specific Anti-IgE
ind Uses Thereof

Indels Length 428;

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Gaps

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168

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RESULT 13
US-10-047-542-45
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US-09-847-208-7
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; OTHER INFORMATION: Fusion between hinge-CH2-CH3; OTHER INFORMATION: (IgE)
US-09-847-208-7
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GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004 CLPI
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 569
TYPE: PRT
                                                                                                                           Sequence 45, Application US/10047542 Patent No. US20020168367A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT (
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
EILE REFERENCE: UC67.002A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Saxon, Andrew APPLICANT: Zhang, Ke APPLICANT: Zhu, Daochen
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Sequence 37, Application US/102145
Publication No. US20030073142A1
GENERAL INFORMATION:
APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Yang, Yong-Min
APPLICANT: Waranktewicz, Theresa
APPLICANT: Chen, Zhong
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US-10-214-524-37
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-45
                                                                                                                                                                                    US-10-214-524-37
                                                                                                                                                                                                                        ; SOFTWARE: PatentIn v
; SEQ ID NO 37
; LENGTH: 574
; TYPE: PRT
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Best Local
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LENGTH: 574
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Best Local
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TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES
FILE REFERENCE: IGE-00101.P.1.1
CURRENT APPLICATION NUMBER: US/10/214,524
CURRENT FILING DATE: 2002-08-08
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/312,120 PRIOR FILING DATE: 2001-08-13 NUMBER OF SEQ ID NOS: 61
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NUMBER OF SEQ ID NOS: 101
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PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
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                                                       FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
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                                     FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
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Barankiewicz, Theresa
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                                                                                                              Conservative
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Pred. No. 1
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Pred. No. 1
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APPLICANT: Ledbetter, Jeffrey A.

APPLICANT: Hayden-Ledbetter, Martha S.

TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 334
LENGTH: 592
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion polypeptide
US-10-207-655-334
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Search completed: July 15, 2003, 07:17:19 Job time: 25.5495 secs
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1707; DB 9; Length 592; Best Local Similarity 100.0%; Pred. No. 1.7e-121; Matches 320; Conservative 0; Mismatches 0; Indels 0
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compug
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    DВ
      US-08-336-583-2

PCT US95-13795-2

US-09-122-545-2

US-08-232-539D-56

US-08-433-105A-6

US-08-433-105A-6

US-08-433-105A-6

US-08-601-184-2

US-08-601-184-2

US-08-232-539D-54

US-08-232-539D-54

US-08-646-981-16

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US-08-646-981-17

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US-08-646-469-13

US-08-765-469-13

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US-08-336-583-2

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid

Query Match Best Local 9 Matches 183

Local Similarity nes 182; Conserv

56.0%; score 956.5; DB 1; ilarity 56.2%; Pred. No. 4.5e-84; Conservative 50; Mismatches 87;

Length 426;

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60 EGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPF 119

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                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                         TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
'REGISTRATION NUMBER: 36,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HOLLIS, GREGORY F. APPLICANT: PATEL, MAYUR D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/13795 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: RAHWAY
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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DLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVG 179
                                                                                                                            FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQ-VMDVDLSTASTTQ 59
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                                                   EGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPF 119
                                                                                                     FIPPTVKLFHSSCNPVGDTHTTIQLLCLISGYVPGDMEVIWLVDGQKATNIFPYTAPGTK
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                                                                                                                                                                          Conservative
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- MO: 2:
                                                                                                                                                                                                                                                                                           single
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56.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  19211Y
                                                                                                                                                                                         Score 956.5; DB 5
Pred. No. 4.5e-84;
                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version
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US-08-232-539D-56
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US-09-192-545-2
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 Sequence 56, Application US/08232539D Patent No. 5965709
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: JP HEI 9-313989
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Taya, Choji
APPLICANT: Matsuoka, Kunie
APPLICANT: Matsuoka, Kunie
TITLE OF INVENTION: Transgenic Animal Allergy Models and
FILE REFERENCE: 79979570
CURRENT APPLICATION NUMBER: US/09/192,545
CURRENT FILING DATE: 1998-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Karasuyama, APPLICANT: Yonekawa, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial
FEATURE: Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 136; Conserv
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                                                                                                                                                                                                                                                                                                            366
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                                                                                                     544 KLEKTISTSLG
                                                                                                                                     309 TVQRAVSVNPG 319
                                                                                                                                                                                                                                           425 VVDRPDFPKPIVRSITLPQVSQRSAPEVYVFPPPE-EESEDKRTLTCLIQNFFPEDISVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 CDGGGHFPPTIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTTQEGELASTQSELT 71
                                                                                                                                                                                                                                                                                                                                                                                                              72 LSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFDLFIRKSPTITC
                                                                                                                                                                       RVTHPHLPRALMRSTTKTS-GPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQ
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                                                                                                                                                                                                                                                                                                           LVVDLESEK-NVNVTWNQEKKTSVSASQWYTKHHNNATTSITSILPVVAKDWIEGYGYQC
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Hiromichi
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GENERAL INFORMATION:

APPLICANT: Presta, Leonard APPLICANT: Jardieu, Paula N TITLE OF INVENTION: IGE Ant

IgE Antagonists

Paula M. 60

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CORRESPONDENCE ADDRESS NUMBER OF SEQUENCES:

Genentech, Inc.

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RESULT 5
US-08-399-106A-6
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                                                                                                                                                                                                                                     Sequence 6, Application US/08399106A Patent No. 5731168
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                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                 GENERAL INFORMATION:
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LENGTH: 113 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
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                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                               APPLICANT: Presta, Leonard APPLICANT: Ridgway, John B.
                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
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                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/OFFILING DATE: 21-Apr-1994 CLASSIFICATION: 530
OMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
                                          CITY: South San Francisco
STATE: California
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                           COUNTRY:
                                                                         STREET:
                                                                                                                                                                                                                                                                                                                         101 CADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTR 160
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                                                                         460 Point San Bruno Blvd
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                             USA
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                                                                                                                                                                                                 Carter, Paul J.
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                                                                                                                                      POLYPEPTIDES
                                                                                                                                                     A METHOD FOR
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US-08-433-105A-6
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--- rocal Similarity
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                              APPLICATION NUMBER: US/08/
FILING DATE: 03-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/399
FILING DATE: 01-MAR-1995
ATTOREY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,00
REFERENCE/DOCKET NUMBER: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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LENGTH: 110 amino acid
                                                                                                                                                                                                                                       SOFTWARE: WinPatin (Ge: CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
APPLICANT: Ridgway, John B.
TITLE OF INVENTION: A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES
NUMBER OF SEQUENCES: 16
               TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 110 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 415/2-
TELEPHONE: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                         SSEE: Genentech, Inc.
T: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                                                                                                                                                                     94080
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415/952-9881
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                                                                                                                                            08/399106
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US-08-434-869A-6
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Best Local Similarity
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MEDIUM TYPE: 3.5 inch, 1.44 Mb:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/3
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Presta, Leonard G.
APPLICANT: Ridgway, John B.
TITLE OF INVENTION: A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES
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nes 110; Conserv
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                                                 211 GPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRK 270
271 TKGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 320
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South San Francisco
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                                 GPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRK 60
                                                                                                                                                                                                                                                                                                                                                                             Lee, Wendy M.
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100.0%; F1
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                                                                                                    Score 587; DB 2; 1; Pred. No. 2.7e-49; 0; Mismatches 0;
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US-08-037-579A-2
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                                                                                                                                                                          Sequence 2, Application Patent No. 6043345
GENERAL INFORMATION:
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Best Local
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TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                   APPLICANT: Zhang, Ke
APPLICANT: Max, Edward E
APPLICANT: Saxon, Andrew
TITLE OF INVENTION: IGE
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CURRENT APPLICATION DATA:
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                                                                     CORRESPONDENCE ADDRESS:
                                                                                      NUMBER OF SEQUENCES:
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STREET: 4 LINC.
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4 Embarcadero Cent
                               E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
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SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:

941114187

COUNTRY:

California

MEDIUM TYPE: Floppy disk

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                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-466-163B-1
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TELEFX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
                                                                                                                                                                            SEQ ID NO 1
LENGTH: 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08466163B Patent No. 6329509
                                                      Matches
                                                                        Query Match
Best Local Similarity
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TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/466,163B CURRENT FILING DATE: 1995-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jardieu, Paula M. APPLICANT: Presta, Leonard
                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 07/744,768 PRIOR FILING DATE: 1991-08-14
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1992-05-07
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 07/879,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 494-8700
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ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PCDOS/MSDOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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GY: linear
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99.1%;
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                                                  Score 566.5; DB 4;
Pred. No. 2.5e-47;
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US-08-464-025A-1
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Sequence 1, Application Patent No. 5994514
GENERAL INFORMATION:
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                                                                                                                                                                                                                                        Matches 105;
                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIF CO...
PRIOR APPLICATION DATA:
08/178583
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CURRENT APPLICATION DATA:
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APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: IgE Antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39. REFERENCE/DOCKET NUMBER:
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FILING DATE: 07-JAN-1994
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5965709
                                                                                                                              168 GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGP 212
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                                                                                                          61 GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGP
                                                                                                                                                                           1 GVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRN
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                                 Application US/08464025A
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14-AUG-1991
                                                                                                                                                                                                                                 32.6%; Scu.
/ 100.0%; Pr
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Pred. No.
                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                       2.5e-46;
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TITLE OF INVENTION: APPLICANT:

Jardieu et al.

IMMUNOGLOBULIN VARIANTS

NUMBER OF SEQUENCES:

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US-08-464-025A-1
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Best Local Similarity
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APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch,
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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LENGTH: 119 amino acids
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 inc
                                                                         PRIOR APPLICATION DATA:
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CTTY: South San !
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                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DO SOFTWARE: WinPatin (Genentech)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATION SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 TRKEEKQR----NGTLTVTSTLFVGTRDWIEGETYQCRVTHPHLPRAL-MRSTTKTSGP 212
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                           1.44 Mb floppy disk
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Pred. No. 2.3e-43;
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INFORMATION FOR SEQ ID NO:
             REFERENCE/DOCKET NUMBER: 1 INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: Svoboda, Craig G.
SEQUENCE CHARACTERISTICS:
                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ONO, YOICHI APPLICANT: TOKIYOSHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                    ADDRESSEE: BIRCH, STREET: PO BOX 747
CITY: FALLS CHURCH
                                            NAME: WEINER, MARC S REGISTRATION NUMBER:
                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/1 FILING DATE: 26-JAN-1994
                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 118 amino acids
TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 TRKEEKQR---NGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRAL-MRSTTKTSGP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 TRKEEKQRXNXXGTLTVTSTLPVGTRDWIEGET-QCRVTHPHLPRALXMRSTTKTSGP 118
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Similarity 89.8%;
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                                                                                                                                                                                                                                                                         VA
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                                                                                                                                                                                                                                                                                                             E: BIRCH, STEWART, KOLASCH AND BIRCH
PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIMACHI, KAZUHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAEDA, HIROAKI
EDA, YASUYUKI
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                                                                                                                                                                                                                                                                                                                                                                                            DOG-MOUSE HETEROHYBRIDOMA AND GENE FRAGMENT CODING FOR CONSTANT REGION OF CANINE
                                                                                                                                                                                                                                                                                                                                                                            IMMUNOGLOBULINS
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                                              32,181
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Pred. No. 1.1e-41;
1; Mismatches 2
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                              1488-106
                                                                                                                                                                Version #1.30
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                       APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
                                                                                                                                                                                                                                SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                               STREET: 419 Sevent
CITY: Washington
                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/436,463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 SVDKSRWQRGDTFICAVMHEALHNHYT-QKSLSHSPGK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 NPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHS-TRKE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 GLYSLSSMYTVPSSRW-SSETFTCNVAHPASKTKVDKPVPKRENGRVPRPPDCPKCPAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 ELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFE-------DSTKKCADS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEG
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                                                                                                                                                                                                                                                                                                                                                                                D.C.
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TOKIYOSHI, Sachio
                                                                                                                                                                                                                                                                                                                                                             USA
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N: 536
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                                                        KIMACHI-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142;
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Best Local 9
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Matches 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
TYPE: a
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  298
                                   284 VTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 320
                                                                                                                   224 PEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLE
                                                                                                                                                                                                                                        118 MLGGPSIFIFPPKPKDTLSISRTPEVTCLVVDLGPDDSDVQITWFVDNTQVYTAKTSPRE
                                                                                                                                                                                                                                                               107 --RGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEE
                                                                                                                                                                                                                                                                                                                      59 GLYSLSSMYTVPSSRWLSD-TFTCNVAHPPSNTKVDKTVRKTDHPPGPKPCDCPKCPPPE 117
                                                                                                                                                                                                                                                                                                                                                            62 ELASTQSELTLSQKHWLSDRTYTCQVTY-QGHTFEDSTKKCADSNP------
                                                                                                                                                                                                                                                                                                                                                                                                    2 TAPSVFPLAPSC--GTTSGATVALACLVLGYFPEPVTVSW-NSGALTSGVHTFPAVLQAS
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   amino acid
   GY: linear
VDRSHWQRGNTYTCSVSHEALHSHHT-QKSLTQSPGK 333
                                                                             AQEELSRNKVSVTCLIKSFHPPDIAVEWEITGQPEPENNYRTTPPQLDSDGTYFVYSKLS
                                                                                                                                                           EQFNSTYRVVSVLPILHQDWLKGKEFKCKVNSKSLPSPIERTISKAKGQPHEPQVYVLPP
                                                                                                                                                                                                 KQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.7%; score 455.5; DB 1; 32.0%; Pred. No. 6.5e-36; tive 59; Mismatches 147;
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283 237 223 177 163

Search completed: July 15, 2003, Job time: 14.8457 secs 07:02:41

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1225
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length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    July 15, 2003, 06:52:29; Search time 32.9929 Seconds (without alignments) 1657.949 Million cell updates/sec
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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3060
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  \begin{smallmatrix} 557 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 257 \\ 25
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Copyright (c) 1993 - 2003 Compugen Ltd.
EHRT
G2EP
I47158
I47161
S38864
S22080
PS0018
G3MSC
C30554
S31459
G3MSM
PC4436
G1MS
PS0017
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147160
147159
147162
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GHHU
S69339
S31866
PT0207
A23511
A60764
G3HUWI
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G2HU
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45	44	43	42	41	40	39	38	37	36	35 5	34	ω G	32	31	30
576	669	731.5	735	746.5	747.5	750	751.5	761	766.5	771	772	776	776	776.5	784.5
18.8	21.9	23.9	24.0	24.4	24.4	24.5	24.6	24.9	25.0	25.2	25.2	25.4	25.4	25.4	25.6
227	180	475	327	405	322	423	474	446	388	399	335	469	330	329	393
Ν	N	N	N	<u></u>	N	Н	ш	N	<u>, , , , , , , , , , , , , , , , , , , </u>	Н	ب	ν	1	N	1
PH1215	I46732	S01321	S06611	G2MSBM	PS0019	EHMSS	G2MS11	S40295	EHMS	G2MSAM	G2MSAB	S37483	G2MSA	S00847	G1MSM
Ig epsilon chain C	Ig gamma heavy cha	Ig gamma-2b chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma-2a chain	Ig epsilon chain C	Ig gamma-2b chain	Ig gamma-2a chain	Ig epsilon chain C	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma∼2a chain	Ig gamma-2a chain	Ig gamma-2c chain	Ig gamma-1 chain C

ALIGNMENTS

Ig epsilon chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 11-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999 C;Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999 C;Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; R;Flanagan, J.G.; Rabbitts, T.H. EMBO J. 1, 655-660, 1982

EHHU RESULT 1

A: Molecule type: protein	
A: Accession: A94418	Io gamma-1 chain C
	monoclonal antibod
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.	
R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.	
A; Note: this sequence difference may be due to polymorphism	
A;Cross-references: GB:J00222; NID:g184755	Ig gamma-3 chain C
A; Residues: 1-358, 'L', 360-428 < MAX>	
A; Molecule type: DNA	Ig heavy chain pre
A; Accession: A90824	
A; Reference number: A90824; MUID:83001945; PMID:6288268	
A; Title: Duplication and deletion in the human immunoglobulin epsilon genes.	gamma 1
Cell 29, 691-699, 1982	gamma-2
R; Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.	epsilon chain
A;Cross-reterences: GB:L00022; GB:J00227; GB:V00555; NID:g185035	
A; Residues: 1-428 <sen></sen>	ig gamma 2a chain
A; Molecule type: mRNA	gamma
A;Accession: A93491	
A; Reference number: A93491; MUID:83168897; PMID:6300763	
A; Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon	Ig gamma-2 chain C
Nucleic Acids Res. 11, 719-726, 1983	gamma-3 heavy
R; Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; S	gamma-3
	ig gamma-3 chain C
A; Residues: 320-428 <zha></zha>	gamma chain C
A; Molecule type: DNA.	gamma-1 chain
A; Accession: PH1214	
A; Reference number: PHI214; MUID:92308839; PMID:1613458	
A; Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splic	epsilon-chain
	Ig epsilon chain C
R; Zhang, K.; Saxon, A.; Max, E.E.	
A;Cross-references: GB:J00222; NID:g184755	Description
A; Residues: 2-428 <ued></ued>	
A; Molecule type: DNA	
A;Accession: A23195	
A; Reference number: A23195; MUID:84207910; PMID:6327276	
A;Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseu	stribution.
EMBO J. 1, 1539-1544, 1982	result being printed,
R; Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.	chance to have a
A;Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035	
A; Residues: 1-428 <fla></fla>	
A; Molecule type: DNA	
A; Accession: A22771	-
A: Title: The sequence of a human immunoglobulin epsilon heavy chain constant region q	
EMBO J. I, 655-660, 1982	

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A;Introns: 1/1; 104/1; 211/1; 319/1
c;Complex: An immunoglobulin heterotetramer subunit consists of two identical light Air disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology <IM1>
f;128-87/Domain: immunoglobulin homology <IM2>
f;128-195/Domain: immunoglobulin homology <IM2>
                                                            F;128-195/Domain: immunoglobulin homology <IM2>
F;232-301/Domain: immunoglobulin homology <IM3>
F;338-407/Domain: immunoglobulin homology <IM3>
F;338-407/Domain: immunoglobulin homology <IM4>
F;147/Disulfide bonds: interchain (to light chain) #status predicted
F;15-105,29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted
F;21,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status
F;121,209/Disulfide bonds: interchain (to heavy chain) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross:references: GB:S53497; NID:g263162; A;Experimental source: B cell myeloma U-266 A;Note: sequence extracted from NCBI backbon C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A46536; MUID:93122085; PMID:8419166 A;Accession: C46536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Cloning and sequence determination of the gene A; Reference number: A93933; MUID:83065234; PMID:6815656 A; Accession: B93933
                                                                                                                                                                                                                                                                                                                                                                  A; Map position:
A; Introns: 1/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type:
A; Residues: 401-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: sequence extracted A; Accession: A46536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts
A;Reference number: A53116; MUID:94103254; PMID:8276835
A;Accession: A53116
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:119335;
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: IGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 382-391 <HE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:S55273; NID:g263166; A;Experimental source: B cell myeloma U-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 382-426 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: myeloma U266-derived cell line AF-10 A; Note: sequence extracted from NCBI backbone (NCBIN:141701,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 320-428 <ZH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 98-352 <I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Purification and characterization of a recombinant human A; Reference number: S02438; MUID:88083554; PMID:3121387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS
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A; Residues: 1-40; 68-114; 427-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Kenten,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Hellman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB:L00022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:S55276; NID:g263168; Experimental source: B cell myeloma U-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: D46536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Experimental source: myeloma protein Nd; Derbyshire, Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire,
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401-428 <HE3>
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Similarity
                                                                                                                                                                                                                                                                                                                                                                                         14q32.33-14q32.33
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57.78;
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Score 1766;
Pred. No. 2
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DB 1;
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Ig epsilon-chain - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 0
                                                           R; Sakoyama, Y.; Hong, K.
Proc. Natl. Acad. Sci. U
                                                                                              C; Accession:
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I36948
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A;Accession: I36948
A;Status: prelimina
                               A; Reference number: I36948;
                                              A; Title: Nucleotide sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGSGGGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS 185
                                                                                                                                                                                                                                        ICRAVHEAASPSQTVQRAVSVNPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PSPEDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                                                                                                                                                                                                                                                                   LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
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                             U.S.A. 84, 1080-1084, 1987 quences of immunoglobulin epsilon 6948; MUID:87147196; PMID:3103123
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                                                                                                             04-Oct-1996
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                                                                                                          #text_change
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                                              genes
                                                of chimpanzee
                                                                                                            21-Jan-2000
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C; Superfamily: im F; 336-405/Domain: A;Introns: 103/1; 209/1; 317/1 C;Superfamily: immunoglobulin C u F;336-405/Domain: immunoglobulin A; Cross-references: A; Molecule type: DNA A; Residues: 1-426 < RES> Query Match Genetics: preliminary; translated from GB/EMBL/DDBJ 186 129 w VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGSGGGGS REPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS RSPSLFPLTRCCKNIPSNATSVTLGCLAMGYFPEPVMVTWDA-GSLNGTTMTLPATTLTP Conservative GB:M15398; 55.7**%**; 76.0**%**; NID:g176797; PIDN:AAA35416.1; 20; region; immunoglobulin homology <IMM> Score 1705.5; Pred. No. 1.3 Mismatches 5; DB 2, 1.3e-98; 62; Indels homology Length PID:g176798 426; 25; Gaps 61 244 8

105 305

STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR

304 161 364

GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA

--SRDFT-PTVKVLQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA

62

SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC

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A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Ruttshauser, U.; Gall, W. Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gal A;Reference number: A90563; MUID:71064024; PM. A;Accession: B90563
A;Molecule +---
  A; Molecule type: protein
A; Residues: 136-154, 'Q',156-165, 'Q',167-176, 'Q',178-194, 'N',196-197, 'D',199-238, 'E'
A; Residues: 136-194, 'Q',156-165, 'Q', 167-176, 'Q',178-194, 'N',196-197, 'D',199-238, 'E'
A; Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
R; Ponsting1, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A; Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein igen Primaerstruktur.
A; Reference number: A91668; MUID:77070269; PMID:826475
                                                                                                                                                                                                            A; Note: this sequence has the Glm(3) marker R; Rutlishauser, U.; Cunningham, B.A.; Bennet Biochemistry 9, 3171-3181, 1970
A; Title: The covalent structure of a human A; Reference number: A90564; MUID:71064025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 88-113; 235-330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Structure of human immunoglobulin A;Reference number: S33887; MUID:83001943; A;Accession: S33887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z17370 R;Takahashi, N.; Ueda, S.; Obata, Cell 29, 671-679, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: Lys-330 is removed after R; Harris, L.J. submitted to the EMBL Data Librar A; Reference number: S33904 A; Accession: S36861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL:Z17370 A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The nucleotide sequence of a human immunoglobulin A;Reference number: A93433; MUID:82274238; PMID:6287432 A;Accession: A93433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999 C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146 R;Ellison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982
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19 gamma-1 chain C region - h
C;Species: Homo sapiens (man)
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A; Residues: 1-96, 'R', 98-135 <CUN>
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A; Residues: 1-330 <ELL>
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Bennett,
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PMID:5530842
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PMID:6811139
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PMID:5489771
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, C.; Konigsberg,
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RESULT 4
$69339

Ig heavy chain V region precursor - human
C; Species: Homo sapiens (man)
C; Date: 19-Mar-1997 #sequence_revision 19
C; Accession: $69339; $72664
R; Khamlichi, A.A.; Aucouturier, P.; Preud
Eur. J. Biochem. 229, 54-60, 1995
A; Title: Structure of abnormal heavy chai
A; Reference number: $69339; MUID:95262687
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associa C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <IMI>F;213-206/Domain: immunoglobulin homology <IMI>F;243-310/Domain: immunoglobulin homology <IMI>F;243-310/Domain: immunoglobulin homology <IMI>F;27-83,144-204,250-308/Disulfide bonds: #status experimental F;103/Disulfide bonds: interchain (to light chain) #status experimental F;103/Disulfide bonds: interchain (to heavy chain) #status experimental F;104/Disulfide bonds: interchain (to heavy chain) #status experimental F;105/Disulfide bonds: anterchain (to heavy chain) #status experimental
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A; Molecule type: protein
A; Residues: 1-34, (0', 36-96, 'K', 98-115, '0', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E'
A; Note: this sequence has the Glm(17) and Glm(1) markers
R; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
HOppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1
A; Reference number: A91723; MUID:83289131; PMID:6884994
A; Contents: myeloma protein KOL; disulfide bonds
A; Accession: A91723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14932.33-14932.33
A;Introns: 99/1; 114/1; 224/1
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A; Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330
A: Note: this sequence has the Glm(3) and Glm(non-1) markers
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A;Title: The covalent structure of a human
A;Reference number: A90555; MUID:71064027;
A;Contents: annotation; disulfide bonds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: this sequence has R; Gall, W.E.; Edelman, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Contents: myeloma
A; Accession: B91668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matchés 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                               181
                                                                                                                                                                                                                                                               159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225;
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                                                                                                                                                                                                                                                                                      NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                         EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                           ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                           NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                           EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                               PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1225; DB 1;
Pred. No. 6.3e-69;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gammaG-immunoglobulin.
PMID:4923144
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MUID:95262687; PMID:7744049 heavy chains

in human heavy-chain-deposition

disease

Preud'homme,

J.L.; Cogne, #text_change

19-Mar-1997

01-Dec

human

Вр

204

PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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R;Filpula, D.
submitted to the EMBL Data Library, February 1993
....rintion: Screeing method for protein-protein
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S31866
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                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-255 <FIL>
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: Screeing method A; Reference number: S31866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: synthetic A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000 C;Accession: S31866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
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A; Accession: S72664
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A; Residues: 1-374 <KHA>
A; Cross-references: EMBL: X81695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                            ;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069; Reywords: immunoglobulin; Reywords: immunoglobulin; 1-22/Region: Escherichia coli outer membrane protein A precursor; 23-255/Region: human Ig gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma-1 chain
Species: synthe
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               Accession: S31866
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PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSSPGK
                                                                                                                                 NWYVDGYEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                              EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                  ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                ESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                            39.88;
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Pred. No. 1
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1.4e-68;
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                                                                                                                                                                                                                                                                             Length 255
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A;Gene: GDB:IGHG3
A;Cross references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3
C;Superfamily: immunoglobulin C region; imm
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
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                                   밁
                                                                                                                                                                               C; Keywords: immu F; 20-85/Domain:
                                                                                                                                                                                                                                                                                                                                                                                R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy cha A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
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Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision
                                                                     Qy
                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-377 < HUC>
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C;Keywords: immunoglobulin
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                                                                                                                                                                                                                                                                                                                               A; Cross-references:
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                                                                                                           Matches
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Best Local
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                                                                                                           208;
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61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70
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                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A23511
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                                                    EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28,
NWYYDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                   EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
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                                                                                                                                                                             immunoglobulin homology <IMM>
                                                                                                           Conservative
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89.7%;
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                                                                                                                                                                                                                                    145/3; 160/3; 270/3
                                                                                                                                                                                                                                                                                                                             GB:M12958; NID:g33070; PIDN:CAA27268.1;
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                                                                                                       Score 1138; DB 2;
Pred. No. 1.9e-63;
1; Mismatches 13;
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PMID:2062315
                                                                                                           13;
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120
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Ig gamma-3 heavy chain disease proteins - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A90219; A90198; A93915; A02149
R;Frangione, B.; Rosenwasser; E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1930
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-A;Reference number: A90442; MUID:81021548; PMID:6774747
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
A;Molecule type: protein
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A;Note: the sequence of residues 42-76 was taken from the reference that follows
R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication A;Reference number: A92219; MUID:77118561; PMID:402363
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G3HUWI
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C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, A; Reference number: A60764; MUID:90007613; PMID:2571587 A; Accession: A60764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        망
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-377 < HUC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain C region, form LAT - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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89.7%;
                chains,
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Pred. No. 2.
                sequence
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             corresponding
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.5e-63;
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                residues
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                0f
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Dete: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma hea
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g
A;Note: Lys-326 is probably removed posttranslationally
A;Nang, A.C.; Tung, E.; Fudenberg, H.H.
                                                                                                                                                                                                                                                                                                                          RESULT
G2HU
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PID:g6066056

heavy chain

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A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule type: protein
A;Rote: this protein lacks most of the V region, all of the CH1 region, and part of the A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the A;Note: a carboxyl chain disease in man: CNA sequence supports partial gene deleting the contents: heavy chain disease protein Omm
A;Accession: A93915
A;Contents: heavy chain disease protein Omm
A;Accession: A93915
A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin; byroglutamic acid C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid F;203-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C. Biochem. Biophys. Res. Commun. 71, 907-914, 1916.
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Struc A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: GDB:IGHG3
A;Cross-references:
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A90198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 12-97 <MIC>
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Best Local
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239
                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                  WYVDGVQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                      NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                   ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                      EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
PMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG
                                                            PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPG
                                                                                                                                   ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP
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88.3%;
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Pred. No. 1.1e-62;
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E.C.
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289
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Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
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                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14932.33-14932.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; elycoprotein; heterotetramer; immunoglobulin
C;Keywords: duplication; elycoprotein; heterotetramer; immunoglobulin
C;Keywords: duplication; elycoprotein; heterotetramer; immunoglobulin
E;20-85/Domain: immunoglobulin homology <IMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 238-275 < HOF>
R; Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A; Reference number: A94591
A; Contents: annotation; Zie, revis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 1-19,'(0',21-57,'Z',59,'A',61-193,'D',195-325.
A; Note: Trp-156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Structural studies of immunoglobulin A; Reference number: A93157; MUID: 69064124; PMJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: A note on the amino acid sequence A;Reference number: A93132; MUID:80114419; A;Contents: Zie A;Accession: A93132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Contents: annotation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 1-24, 'E', 26-57, 'EV', 60-85; 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The amino acid sequences of the three heavy A;Reference number: A90752; MUID:80001357; PMID:11306 A;Contents: myeloma protein Zie A;Accession: A90752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Contents: myeloma
A; Accession: A92809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:IGHG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: the revised sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Hofmann, T.; Parr, D.M. Mol. Immunol. 16, 923-925,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: this sequence has since been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Milstein,
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                        103,106,109/Disulfide bonds: interchain (to heavy chain) #status /Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The primary structure
                                                                               121
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                                                                                                                                                 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                        EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                               ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                               ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                         NWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKT
                                                                                                                                                                                                                  ERKCCVE----CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
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Til
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                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                       Score 1107;
Pred. No. 1
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that shown in
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PMID:5782707
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PMID:118920
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PMID:113060
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in having
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C:Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 24-Apr-1984 #sequence_revision 15 Nov-1984 #t C:Accession: A91749; A90290; A93928; A90245; A94416; R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G. Immunogenetics 18, 387-397, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Homo sapiens (man)
C; Date: 02-Apr-1982 #sequence_revision
C; Accession: A9933; A90249; A02150
R; Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
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C; Species: Homo
                                                                                                                      Ig gamma chain C region -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-327 <ELL>
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Best Local
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F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,141-201,247-305/Disulfide bonds: #status predicted F;106,109/Disulfide bonds: interchain (to heavy chain) #status experim F;177/Binding site: carbohydrate (Asn) (covalent), #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: the sequence was determined from the germline ger R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hain disulfide bonds. In some cases, such as IgA and IgM, the subunits C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-65/Domain: immunoglobulin homology <IMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Nucleotide sequence of a human immunoglobulin A; Reference number: A90933; MUID:83157104; PMID:6299662
                          191 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                             71 NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                  11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70
                                                                                                                                                          PQYYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFF 190
                                                                                                                                                                                                                                                NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE
                                                                                                                                                                                                                                                                                                                                                                          LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
                                                                                                                         POVYTLPPSQEEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
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Pred. No. 5.5e-61;
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into

#text_change A02161

16-Jul-1999

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A;Molecule type: protein
A;Residues: 132-143, E',145-161 <FRU>
A;Residues: 132-143, E',145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
Hill, R.L.; Lebovitz, H.E.; Fellows Jr., ed., pp.109-127, Almqvist and Wiksell,
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A;Reference number: A94416
A;Reference number: A94416
A;Reference number: A94416
A;Residues: 129-131;155-172, 'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',
A;Rote: this has the elf allotypic marker, 185-Ala
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaphain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-82/Domain: immunoglobulin homology <IM1>
F;236-303/Domain: immunoglobulin homology <IM3>
F;373/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Reference number: A917-
A;Reference number: A91749
A;Molecule type: mRNA
A;Residues: 1-323 <BER>
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A; Cross references: GB: M16426; NID: g165111; PIDN: ANA31299.1; PI
A; Note: this sequence has the d11 allotypic marker, 104-Met, an
R; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Blochem. J. 116, 249-259, 1970
A; Title: Sequence studies of the Fd section of the heavy chain
A; Reference number: A90245; MUID: 70110015; PMID: 5461106
A; Accession: A90245
RESULT
I47160
Ig gamm
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A; Title: Heavy chain genes of rabbit IgG; isolation of a cDNA A; Reference number: A93928; MUID:83299917; PMID:6193512
A; Accession: A93928
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A; Residues: 1-47, 'E', 49-71, 'PV', 72-128 < PRA>
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J. 151, 337-349, 1975
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      2Ъ
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    chain
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                                                                                                                                                                                                                                                               KCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
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                                                                                                   SISRSPGK
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                                                                                                                                                                                  EWEKNGKAEDNYKTTPAVLDSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQK
                                                                                                                                                                                                     EWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQR
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      constant
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    region
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Pred. No. 1e-47;
  pig
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    (fragment)
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C;Genetics:
                                                                                                                  Qy
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                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                    A;Gene: IgG2a
C;Superfamily: im
F;133-202/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Five putative subclasses of swine A;Reference number: 147158; MUID:95015845; A;Accession: 147159
A;Status: preliminary; translated from GB/E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Kacskovics, I.; Sun, J.; Butler, J.E. J. Immunol. 153, 3565-3573, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Sus scrofa domestica (domest
C;Date: 21-Feb-1997 #sequence_revision
C;Accession: I47159
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147159
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A; Residues: 1-328 < KAC>
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R; Kacskovics, I.; S
                                   Qγ
                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-328 < KA
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Best Local Similarity
Matches 157; Conser
                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                 165 TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE
                                                                                                                                                                                                                                             157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                  11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
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                      PQVTTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS
                                                                                                                                                              CPICPACE-SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH
                                                                                                        NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE
    PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT
                                                                                                                                                                                                                                                                                                                    immunoglobulin C I
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                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: U03779;
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32;

Score 868.5; DB 2 Pred. No. 8.4e-47; 2; Mismatches 32

32;

Indels

ω •-

Gaps

164

284

224 130 2

Length

region; immunoglobulin homology <IMM>

NID: g433123; PIDN: AAA52217.1;

PID:g433124

GB/EMBL/DDBJ

IgG identified PMID:7930579

from

the

cDNA sequences

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A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin
F:133-202/Domain: immunoglobulin homology <IMM>
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C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997
chain constant region - pig (fragment)
Sus scrofa domestica (domestic pig)
Feb-1997 #sequence_revision 21-Feb-1997
                                                                                                                                                                                                                                                                                                                                        NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                          CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                                     FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                     PQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS 188
                                                                                                                                                                                                                                                                                                                  TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE
                                                                                                                                                                                                                                                                                                                                                                                                     CPICPACE-SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH
                                                                                                                                                                                                                               PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT
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70.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 8.4e
2; Mismatches
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No. 8.4e-47;
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  #text_change
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    21-Jan-2000
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Search completed: July 15, 2003, 06:59:33 Job time: 33.9929 secs
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Accession: 147162
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A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.3%; Score 865; DB 2; Length 277; Best Local Similarity 69.0%; Pred. No. 1.1e-46; Matches 158; Conservative 32; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                              184 DSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
| | |:|||||| |||:||:|||:||||||||||||:|::|||
| 229 DVDGTYFLYSKLAVDKASWQRGDTFQCAVMHEALHNHYTQKSIFKTPGK 277
                                                                                                                                                                        49 TKTKPPCPICPACEGPGPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQFSWYVD 108
                                                                                                                                                                                                                                                                                                                                                                                 8 THTCPPCP-APELIG-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Gapop 10.0 ,
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3060
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                                                                           "The covalent structure of a hu Intrachain disulfide bonds."; Biochemistry 9:3188-3196(1970).
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MEDLINE=71064025; PubMed=5530842;
Rutishauser U., Cunningham B.A.,
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MEDLINE=77070267; |
Dreker L., Schwarz
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MEDLINE=71064027;
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PubMed=1002129;
z J., Reichel W.,
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
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and its complex with fragment B of protein
aureus at 2.9- and 2.8-A resolution.";
Biochemistry 20:2361-2370(1981)
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A02146; GHHU.;
; IFC1; 15-JUL-92.;
; IFC2; 15-JUL-92.
ew; HGNC:5525; IGHG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STANDISCELLANEOUS: EU ALSO DIFFERS IN THE A
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SM00410; iG_like; 1.
SM00407; iGc1; 2.
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REMOVED POST-TRANSLATIONALLY.

K -> R (IN G1M(3) MARKER).

/FTId=VAR_003886.

D -> E (IN G1M(NON-1) MARKER).

/FTId=VAR_003887.

L -> M (IN G1M(NON-1) MARKER).

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MEDLINE-81021548; PubMed=6774747;

Frangione B., Rosenwasser E., Prelli F., Franklin E.

"Primary structure of human gamma 3 immunoglobulin c
gamma 3 heavy-chain disease protein Wis.";

Biochemistry 19:4304-4308(1980).
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 REVISIONS TO 12-97 (PROTEIN WIS).
MEDILTNE-77118561; PubMed-402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
"Primary structure of the 'hinge' region of h
quadruplication of a 15-amino acid residue ba
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Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

INTERCHAIN DISULFIDE BY 12 DISULFIDE BONDS; IT HAS AN INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO NORMALLY PRESENT IN THE HINGE REGION.

I- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS

MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKE REF. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/orsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC). MEDILINE-77021516; PubMed-823945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E. "The amino acid sequence of 'heavy chain disease' protein Structure of the Fc fragment of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced currently selections and the Ebetween the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no rest the European Bioinformatics Institutions as long as its content.
                                                                                                                                                                                                                                                                    SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:5527; IGHG3 MIM; 147120; -.
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InterPro; IPR003600;
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MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCLASS.

MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
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                                                                                                                                                                                                                                                                                            PF00047; 1g; 2
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Heavy chain disease in man: cDNA sequence supports partial
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P01859;
                                    Takahashi N., Ueda S., Obata M., N.
"Structure of human immunoglobulin
evolution of a gene family.";
Cell 29:671-679(1982).
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"Linkage and sequence homology of two human immunoglobulin apnes.";
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Mammalia; Eutheria;
                                                                                                   TISSUE=Fetal liver;
MEDLINE=83001943; PubMed=6811139;
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  MEDLINE-84235992;
             TISSUE-Fetal
                         SEQUENCE OF 99-177 AND 310-326 FROM
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S -> N (IN OMM).
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REVISIONS TO
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"The primary structure of a human 1962 hea
evolutionary, and functional implications.
J. Immunol. 125:1048-1054(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neavy chain genes and genes.";
                                       InterPro; IPR003600; 19_11N0
Pfam; PF00047; 19; 3.
Pfam; PF000410; IG_11ke; 1.
SMART; SM00407; IGC1; 2.
SMART; SM00407: IGC1; 2.
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=72033500; PubMed=4940472;
Milstein C., Frangione B.;
"Disulphide bridges of the heavy chain
Biochem. J. 121:217-225(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stoppini M., Beliotti V., Negri A., "Characterization of the two unique immunoglobulins.";
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"The amino acid sequences of the three h
domains of a human IgG2 myeloma protein.
Can. J. Biochem. 57:758-767(1979).
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                                                                                                                                                                                                                                                                                                            MEDLINE=69064124; PubMed=5782707; Frangione B., Milstein C., Pink J.R.L.; "Structural studies of immunoglobulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A note of the amino acid sequence immunoglobulins gamma chains."; Mol. Immunol. 16:923-925(1979).
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                                                                                                                                     Genew;
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                      PS00290; IG_MHC; 2.
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IPR003600; Ig_like.
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use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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21-JUL-1986 (Rel. C
16-OCT-2001 (Rel. 4
Ig gamma-4 chain C
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Homo sapiens (Human).
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MEDLINE=83157104; PubMed=6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin DNA 1:11-18(1981).
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                                                                                                                                                                                                          MEDLINE-70207560; PubMed-4192699;
MEDLINE-70207560; PubMed-4192699;
Pink J.R.L. Buttery S.H. de Vries G.M.,
"Human immunoglobulin subclasses Partial
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_RABIT
               SEQUENCE OF 1-128.
MEDLINE=76135469; Puratt D.M., Mole L.F.
"Sequence studies or
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P01870;
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                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=84030930; PubMed=
Bernstein K.E., Alexander
                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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SM00407; IGC1; 2.
E; PS00290; IG_MHC; 2.
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                               PubMed=1243651;
L.E.;
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[3]
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Mammalia; Eutheria; Rodentia;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig epsilon chain C region.
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P01862;
21-JUL-1986 (Rel. 0)
21-JUL-1986 (Rel. 0)
15-JUL-1999 (Rel. 38
Ig gamma-2 chain C r
                                                                                                                                                                                                                                                                               Birshtein B.K., Hussain Q.Z., Cebra J.J.; "Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). 3. Amino acid sequence of thalf-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
                                                                                                        "Structure of heavy chain from strain 13 guin immunoglobulin-G(2). II. Amino acid sequence and hinge region cyanogen bromide fragments." Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cavia porcellus (Guinea
Tracey D.E., Cebra J.J
"Primary structure of
                                        SEQUENCE OF 134-226.
MEDLINE=75036072; PubMed=4429665;
                                                                                                                                                                                             Turner K.J.,
                                                                                                                                                                                                                  MEDLINE=71058486; PubMed=5538616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1975) to
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                                                                                                                                                                                                                                        SEQUENCE OF 69-133 AND 312-329
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-71058471;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 4-68.
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                                                                                                                                                                                                Cebra J
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01, Last sequence up
38, Last annotation
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Rodentia;
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the CH2 homology region
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1; Mismatches
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Hystricognathi; Caviidae;
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EPC_MOUSE STANDARD; PRT; 421 AA.

AC P06336; P01856;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g epsilon chain C region.
OS Mus musculus (Mouse).
OC Eŭkaryota; Metazoa; Chordata; Craniata; Vertebra
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muri
OX NCBL_TaxID-10090;
RN (11).
RP SEQUENCE FROM N.A.
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Best Local :
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SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea
Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003600
Pfam; PF00047; ig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Primary structure of the CH3 homology region antibodies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=71058474;
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InterPro; IPR003600; Ig_like
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A02151; G2GP.
; P01842; 7FAB.
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3; Mismatches
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                                                         Craniata; Vertebrata;
Sciurognathi; Muridae
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A HEAVY CHAIN).
A HEAVY CHAIN).
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and this statement is not removed.
requires a license agreement (See
an email to license@isb-sib.ch).
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
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RESULT 11
GC3_MOUSE
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Best Local :
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between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
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MEDLINE=85027161; PubMed=6092053;

MEDLINE=85027161; PubMed=6092053;

Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez

Tucker P.W., Blattner F.R.;

"Structural analysis of the murine IgG3 constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Ol-AuG-1991 (Rel. 19, Last sequence
16-CCT-2001 (Rel. 40, Last annotation
Ig gamma-3 chain C region, secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P22436;
01-AUG-1991
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Transmembrane; Alternative splicing.
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                                                                                                                                                                             PS00290; IG_MHC; 1.
                                                                                                      KGLVRKPQVYVMGPPTEQLTEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVMD
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                 QTPQVYTIPPPREQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGT
                                                    REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGS
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19, Last sequence update)
40, Last annotation update)
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64.7%;
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Pred. No. 5.0
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CH2.
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P03987;
23-OCT-1986
01-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003600; Ig_lik
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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Tucker P.W., Blatther F.R.;
"Structural analysis of the murine
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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InterPro; IPR003597;
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                          PPGSSCPPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKE 165
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; Ig_cl.
; Ig_like.
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POTENTIAL.
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E -> Q (IN RE
E -> P -> F (IN RE
                                                                                                                                        Score 801.5; DB : Pred. No. 4.1e-48
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21-JUL-1986
30-MAY-2000
EMBL; V00793; CAA24172.1; -. EMBL; V00793; CAA24173.1; -. EMBL; V00793; CAA24174.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-80202559; PubMed-6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., S
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene
cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
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                                                                                                                                                                                                                                                                                                                  murine myeloma
J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and complete nucleotide sequence gamma 1 chain gene.";
Cell 18:559-568(1979).
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Mammalia; Eutheria;
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                                                                                                                                                                                                              Biochem. J.
                                                                                                                                                                                                                                               Svasti J., Milstein
                                                                                                                                                                                                                                                               MEDLINE=73008889;
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE (MYELOMA MEDLINE=78242288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 70-322 FROM N.A. (MYELOMA MEDLINE-80012837; PubMed-113776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 76-324 FROM N.A.
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Takahashi N., Mano Y.;
                                                                                                                                                                                                                                                                                                                                                     "Evolution of
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an email to license@isb-sib.ch).
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253:6068-6075(1978).
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01, Last sequence up
39, Last annotation
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Sciurognathi; Muridae;
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                                                                                                                                       restrictions
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Brueggemann M.;
Brueggemann M.;
"Evolution of the rat im
Gene 74:473-482(1988).
PIR; PS0017; PS0017.
PIR; PS0017; PS0017.
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EMBL; V00795; CAA24
PIR; A02159; G1MS.
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SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                       GC1_RAT STANDARD; PRT; 326 AA. P20759; O1-FEB-1991 (Rel. 17, Created) O1-FEB-1991 (Rel. 17, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15 gamma-1 chain C region.
                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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InterPro; IPR003006; Ig_MHC
InterPro; IPR003597; Ig_c1.
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                                                                                               SEQUENCE FROM N.A. MEDLINE=89232738;
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FSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK
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Pred. No. 2.1
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N -> D (IN REF. 3).
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Sciurognathi;
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SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC;
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                                                                                     KTISKPEGRTQVPHVYTMSPTKEEMTQNEVSITCMVKGFYPPDIYVEWQMNGQPQENYKN
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RESULT 15
GCIM_MOUSE
ID GCIM_M
AC PO1869
DT 21-ULL
DT 01-NUG
DT 30-MAY
DE Ig gammal
OC Eukary
OC Mammal
OC Mammal
OC MAMMA
RN NCBL_T
RN (1)
RA HONJO
RA HONJO
RA HONJO
RA TAKAHA
RT Gamma
RT Gamma
RT Gamma
RT (2)
RP SEQUEN
RA TYLER
RP SEQUEN
RA TYLER
RT CONSET
RT GOMS
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21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last seque
30-MAY-2000 (Rel. 39, Last annot
Ig gamma-1 chain C region, membr
Mus musculus (Mouse)
                                                                                                                                                           SEQUENCE OF 323-393 FROM N.A.
MEDLINE-#82197626; PubMed-6804950;
Tyler B.M., Cowman A.F., Gerondakis
"MRNA for surface immunoglobulin gan
conserved transmembrane sequence and
   SEQUENCE OF 323-366 FROM N.A. MEDLINE=82115295; PubMed=6799207;
                                                                                                                                                                                                                                                                                                                                                           "Cloning and complete nucleotide gamma 1 chain gene."; Cell 18:559-568(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Honjo T., Obata M., Ya
Takahashi N., Mano Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=80045036; PubMed=115593;
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                                     SEQUENCE OF
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Rodentia;
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annotation update)
membrane-bound for
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                                                                                                   79:2008-2012(1982)
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and a
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a chains encodes
a 28-residue intr
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Query Match
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Matches 135
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InterPro; IPRO03597; Ig_c1.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGc1: 2
PROSITE: PCCC.
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EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
PIR; B02159; GIMSM.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WARDLINE-82222190; PubMed-6283537;
Yamawaki Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.",
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANES
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SPERARTE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains."; cell 26:19-27(1981).
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Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
liternative splicing; Transmembrane.
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212 TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNT
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135; Conserv
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                                TISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
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INTERCHAIN (
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4CC88343B7A1CE27 CRC64;
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180 PPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPG
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272 QPIMNTINGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
     323
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Search completed: July 15, 2003, 06:58:21 Job time : 18.7654 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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1833.165 Million cell updates/sec
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235	301.5	302.5	305	309.5	311	13.5	317	319.5	320	22.5	24.5	326	326.5	334	335	336.5	340	344	44.5	354	356	399	413	435	438	39.5	39.5	40.5
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ALIGNMENTS

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181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232	360 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 419	121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180	300 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 359	61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120	240 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 299	1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60	Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	40.0%;	SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;	Hypothetical protein.	EMBL; BC024289; AAH24289.1;	Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.		TISSUE=SPLEEN;	SEOUENCE FROM N.A.		Mahhhatta; Euchetta; Filhaces; Cacailhith; Homilhidae; Homo. NCBT TaxTD=9606:	Chordata;		Hypothetical 51.8 kDa protein.	01-JUN-2002 (TremBLrel. 21, Last annotation update)	01-JUN-2002 (TremBLrel. 21, Created)		Q8TC77 PRELIMINARY; PRT; 471 AA.	IT 1

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420

PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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RESULT 3
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PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS01187; EGF_CA; UNKNOWN_1.

PROSITE; PS00118; GLU_CARBOXYLATION; UNKNOWN_1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

PROSITE; PS00240; TRYPSIN_DOW; 1.

PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_ESE; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001881; EGF_Ca
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001254; Ser_pro
InterPro; IPR000294; VitK_de
Pfam; PF00008; EGF; 2.
Pfam; PF00008; EGF; 2.
Pfam; PF00099; trypsin; 1.
SMARR; SM00181; EGF; 2.
Q8TC63;
Q8TC63;
01-JUN-2002
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PROSITE; PS01022; EGF_1; UNKNOWN_1.
PROSITE; PS011B6; EGF_2; UNKNOWN_1.
PROSITE; PS011B7; EGF_CA; UNKNOWN_1.
PROSITE; PS011B7; EGF_CA; UNKNOWN_1.
PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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InterPro; IPR000561; EGF-1ike.
InterPro; IPR000742; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR0013006; Ig_MHC.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
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01-DEC-2001 (TrEMBLITE1. 19, Last
01-MAR-2002 (TrEMBLITE1. 20, Last
Factor VII active site mutant imm
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225; Conserv
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Natl. Acad. Sci. I
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                                                                                                                                                               NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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701 AA;
  (TrEMBLrel.
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                                                 PRELIMINARY;
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Pred. No. 2.8e-94;
3; Mismatches 4
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                                                                                                                               InterPro; IPR003006;
Pfam; PF00047; ig; 2
                                                                                                                                                                                                                       Wagner B., Overesch G., Sheoran A., Holmes
Leibold W., Radbruch A.;
"Organization of the equine immunoglobulin
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98383416; PubMed=9717671;
                                                                                                                                                                                                                                                                                                                                                                                                                    Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                      EMBL;
                                                                                                                                                                                                        genes. III. Alignment
                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                genes. III. Alignment of c-mu, c
Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
                                                                                                                                                                                                                                                                                                                                                         Wagner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment).
IGHC1.
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   al Similarity
157; Conserv
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PS00290; IG_MHC; UNKNOWN_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
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473 AA; 5
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67.7%;
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90.5%;
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   36;
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Last annotation
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 Score 877.5;
Pred. No. 1.6e
36; Mismatches
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Pred. No. 9.
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                                                                          A60BF2B01DEFD1F6
                                                                                                                                                                                                      c-gamma,
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les 36;
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                                      Length 337;
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Hypothetical protein
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                                                                                                                             Q99LC4 PRELIMINARY; PRT; 463 AA. Q99LC4; C1-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence up 01-JUN-2002 (TrEMBLrel. 21, Last annotation Similar to RIKEN CDNA 1810060009 gene.
                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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469 AA; 5
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Pred. No. 1.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    534793F155D05457 CRC64;
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Best Local S
Matches 137
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InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003600; Ig_NHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00400; IGc1; 2.
SMART; SM00410; IGc1; 2.
SMART; SM00410; IGc1; 1.
SMART; SM00410; IG_11ke; 1.
SMART; SM00410; IG_11ke; 1.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Wilde K.G., Yu X., Ekramoddoullal

"Cloning of cDNAs encoding for an
antibody (Mab 7, its light and h
single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL,
EMBL; AF152372; AAD40243.1; ".
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9R1A4 PRELIMINARY;
Q9R1A4;
01-MAY-2000 (TIEMBLrel. 13, C
01-MAY-2000 (TIEMBLrel. 13, I
01-JUN-2002 (TIEMBLrel. 21, I
Gammal heavy chain of Mab7 (F
PROSITE;
NON_TER
NON_TER
SEQUENCE
                                                       Interry, ..., 19; 4.
Pfam; PF00047; ig; 4.
SMART; SM00410; IG_11ke; 2
SMART; SM00410; IG_11ke; 2
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Mammalia; Eutheria; Rodentia;
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD;
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EMBL; BC003435; AAHO:
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGH-4.
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                                                                                                                                                                                              InterPro;
                                                                                                                                                                       [nterPro;
                                                                                                                                 # Art.

P; P01842; 7kAb.

J; MGI:96446; Igh 4.

terPro; IPR003600; Ig_like.

harPro; IPR003006; Ig_MHC.
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  437
437 1
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463 AA; 51007 MW; EAA67
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    ΑĄ,
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                                                                                                                                                                                                                                                                                                                                                                   Ekramoddoullah
    48142 MW;
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58.8%;
                                                                UNKNOWN_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Pred. No. 2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                    lah A.K.M., Misra S.;
anti-white pine blister
heavy chains) and constr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAA674C6BBC30783 CRC64;
  5C3A7BB3EE7D697C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on update)
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                                                                                                                                                                                                                                                                                                                           construction
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Gaps

410

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RESULT 8
Q9D8L4
ID Q9D8
AC Q9D8
AC Q9D8
DT 01-J
DT 01-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RA Hayashizaki Y.,
RA Hayashizaki Y.,
RA Hayashizaki Y.,
Ra Kanda Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
Ra Kanda Y., Kawaji H., Kohtsuki S.,
Ra Hayashizaki Y.,
Ra Kanda Y., Kawaji H., Kohtsuki S.,
Ra Hayashizaki Y.,
Ra Kanda Y., Kawaji H., Kohtsuki S.,
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Best Local :
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                                                                                                                                    Atta.

ARGU.

ARGU.

HSSP; PO1842; /..

HSSP; PO18443; Igh-1.

MGD; MGI:96443; Igh-1.

InterPro; IPR003599; Ig.

InterPro; IPR003597; Ig_cl.

"""O; IPR003600; Ig_like.

""O; IPR003006; Ig_MHC.
""AG; Ig_V.
                          InterPro; IPR003006; Ig_M;
InterPro; IPR003596; Ig_V,
Pfam; PF00047; Ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00400; IGc1; 3.
SMART; SM00406; IGc1; 3.
SMART; SM00406; IGv 1.
SMART; SM00410; IG_like; 1
                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9D8L4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=PANCREAS; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19, 18, 1006009Rik protein.
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nes 136; Conserv
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                             IGv; 1.
IG_like; 1.
IG_MHC; UNKNOWN_1
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Rodentia;
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Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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annotation update)
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Matches 141
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InterPro; IPR003600; Ig_like.

InterPro; IPR003600; Ig_like.

InterPro; IPR003596; Ig_wHC.

InterPro; IPR003596; Ig_w.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 3.

R SMART; SM00409; IG; 2.

SMART; SM00407; IGcl; 3.

R SMART; SM00406; IGv; 1.

R SMART; SM00410; IG_like; 1.

R PROSITE; PS00290; IG_MHC; UNKNOWN_1.

R PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2001)
EMBL; BC003878; AAHO:
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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                            FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                              YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
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                                                                                                              REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGS
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Rodentia;
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60.5%;
                                                                                                                                                                                                                                                                                                                                                               25.2%; Score 772; DB 1 62.9%; Pred. No. 2e-56; Live 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ME.
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Pred. No. 2.
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Sciurognathi; Muridae;
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AC Q99L2

AC Q99L2

AC Q99L2

DT 01-U

DT
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Best Local S
Matches 141
                                                                                                                                                                                                                                                                                                                                                  Q91Z05 PRELIMINARY;
Q91Z05;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Hypothetical 51.9 kDa pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q99L25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 1g; 3.

SMART; SM00409; IG; 2.

SMART; SM00407; IGC1; 3.

SMART; SM00406; IGV; 1.

SMART; SM00410; IG_Hike; 1.

PROSITE; PS00290; IG_HMC; UNKNOWN_1.

PROSITE; SM00410; AA; 52449 MW; BE9889B7986DA155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (FEB-2001)
EMBL; BC003888; AAH03
HSSP; P01842; 7FAB.
                             Strausberg R.;
Submitted (JUL-2001) to the
Submit BC010327; AAH10327 1;
                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                              AU044919.
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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      MGI:2144967; AU044919
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); IPR003597; Ig.cl.

); IPR003600; Ig.like.

); IPR003006; Ig_MHC.

); IPR003596; Ig_V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPP--CPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTISKPKGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.2%;
                                                                                                                                                                                                                                                                                                                                                        protein.
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19,
21,
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                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 772; DB
Pred. No. 2e-5
31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                     EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                          Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473
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Murinae; Mus
                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                              Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232
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RESULT 13
Q8VCX7
ID Q8VCX
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Q8R3H6
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Best I
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Best Local
                                                                                                                                                                                                                                     Matches
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Q8R3H6; Q8R3H6; 21, Crea
O1-JUN-2002 (TrEMBLrel. 21, Last
O1-JUN-2002 (TrEMBLrel. 21, Last
Hypothetical 51.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3:
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 473 AA; 5
                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL; BC025447; AAH25447.1; -.
Hypothetical protein.
SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874
                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                          Match
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                                                       416
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                                                                                                                                                                                         236
                                                                                                                                                                                                                                    140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
                                                                                                 EDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKAL
                                                                                                                                                                                                   EPKSCDKT-HTCPP------CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSFGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPIEKTISKAKVQPREPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPSGP I STINPC PPCKECHKC PAPNLEGGP SVF I FPPNIKDVLM I SLTPKVTCVVVDVSE
                                                      PSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTE
                                                                                                                                                                                         EPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSE
                                                                                                                                                                                                                                    Conservative
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IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                             24.6%;
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58.6%;
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                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                  Score 752.5;
Pred. No. 8.7e
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                   Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                               Craniata;
                                                                                                                                                                                                                                                                               8608B57C6CD2874A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                              Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                              .7e-55;
                                                                                                                                                                                                                                                                                                                                                                                                              on update)
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                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                    . 56;
                                                                                                                                                                                                                                                                                                                                                                     Muridae;
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                                                                                                                                                                                                                                                                                                               databases
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                                                       474
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Q8VCX7

PRELIMINARY;

PRT;

613

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RESULT
Q9BQB8
ID Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
DT 01
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Best Local
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Interpro; IPR003597; Ig. cl.
Interpro; IPR003006; Ig.MHC.
Interpro; IPR003506; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBVCX7;
01-MAR-2002 (TrEMBLrel. 20, Crea 01-MAR-2002 (TrEMBLrel. 21, Last 01-JUN-2002 (TrEMBLrel. 21, Last Hypothetical 67.9 kDa protein. Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cr Mammalla; Eutheria; Rodentia; Sc
Q9BQB8;
Q1-UUN-2001 (TrEMBLrel. 17, Created)
Q1-UUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1Rhown (protein for MGC:1905) (protein for MGC:1228).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 613 AA; 6
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                                                                                                                                                           F-EDSTKKCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASG
                                                                                                                                                                                   TKGS-GF-FVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAV
                                                                                                                                                                                                                           RAAPEVYAFATP--EWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRK
                                                                                                                                                                                                                                                                                      KPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGP
                                                                                                                                                                                                                                                                                                                                                                        VSWLKDGKLVESGFTTDPVTIENKGSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLT
                                                                                                                                                                                                             HKHPPAYYLLPPAREQLNLRESATYTCLYKGFSPADISYQWLQRGQLLPQEKYYTSAPMP
                                                                                                                                                                                                                                                                 EPLETKIKIMESHPNGTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISKPNEV
                                                                                                                                                                                                                                                                                                                      FLKNVSSTCAASPSTDILTFTIPPSFADIFLSKSANLTCLVSNLATYE-TLNISWASQSG
                                                                                                                                                                                                                                                                                                                                                                                         ITWLEDGQVMDVDLSTASTTQEGELASTQ-----SELTLSQKHWLSDRTYTCQVTYQGHT::||:||; || ||:||:||
                                                                                                                                                                                                                                                                                                                                                                                                                                  IPAVAE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQGIRTFPTLRTGGKYLATSQVLLSPKSILEGSDEYLVCKI-----HYGGKNRDLHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TPPVLDSVGSFFLYSKLTVDKSRWQQGN--VFSCSVMHEALHNHYQQRSLSLS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       -PGKVEGGGGSGGGGGGSFTPPTVKILQSSCDG-GGHFPPTIQLLCLVSGYTPGTIN
                                                                                          PRELIMINARY;
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28.5%;
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Last annotation update)
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Sciurognathi; Muridae;
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Matches
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SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 4.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_1ike; 1.
PROSITE; PS00290; IG_MHC; UNKNOI SEQUENCE 597 AA; 65300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003597;
InterPro; IPR003600;
InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2001) to the EMBL; BC006180; AAH06180.1; EMBL; BC001872; AAH01872.1; HSSP; P01825; 7FAB.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
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Mammalia; Eutheria;
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SILTVSEEEWNTGETYTCVVAHEAL-PNRVTERTVDKSTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPKDTLMISRTPEVTCVVVDVS-----HEDPEVKFNWYVD----GVEVHNVKTKPR
                                                  PAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAH
                                                                          ATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVF
                                                                                                                   KQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-
                                                                                                                                                                       SNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEE
                                                                                                                                                                                                                                 VDLSTASTTQEGELA----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCAD
                                                                                                                                                                                                                                                                                                                                          PVLDSVGSFFLYSKLTVDKSRWQQG--NVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGG
                                                                                                                                                                                                                                                                                                                                                                     SASAPTLFPLVSCENSPS----DTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFP
                         SRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK
                                                                                                     SHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLP
                                                                                                                                                         DQDTAIRVFAIPPSFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISE
                                                                                                                                                                                                             SGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVP
                                                                                                                                                                                                                                                                                   SGGGGSGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SLTCGVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGITNYNPSLKSR
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Pred. No. 1.
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.7e-29;
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Best Local Similarity
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SMART; SM00409; IG; 2.

SMART; SM00407; IGC1; 4.

SMART; SM00406; IGV; 1.

SMART; SM00410; IG_11ke; 1.

PROSITE; PS00290; IG_MHC; UNKNOWN_3.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
101-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 65.3 kDa protein.
Hypothetical 65.3 kDa protein.
Eukoryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HSSP; P01825; 7FAB.
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SEQUENCE 5
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Interpro; IPR003597; Ig_cl.
Interpro; IPR003600; Ig_like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
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480 PAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVLDSVGSFFLYSKLTVDKSRWQQG--NVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPKDTLMISRTPEVTCYVVDVS-----HEDPEVKFNWYVD----GVEVHNVKTKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPREPQVYTL-----PPSRDELTKNQVSLTCLVKGFYPSDIAVEWE-SNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                           SGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEQYNSTYRVVSVLTVLHQNWMNGKEYKC-KVSNKALPAPIEK-----TISKAKV 126
                                                     ATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FFVF
                                                                                                           SHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLP
                                                                                                                                                  KQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF-
                                                                                                                                                                                                                             DQDTAIRVFAIPPSFASIFLTKSTKLTCLVTDLT-TYDSVTISWTRQNGEAVKTHTNISE
                                                                                                                                                                                                                                                                                  SNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEE
                                                                                                                                                                                                                                                                                                                                                                                                    VDLSTASTTQEGELA----STQSELTLSQKHWLSDRTYTCQVTYQGHTF-EDSTKKCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVLRG-GKYAATSQVLLPSKDVMQGTDEHVVCKVQHP---NGNKEKNVPL-PVIAE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             -------LPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVG
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597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
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Search completed: July 15, 2003, 07:01:49
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Title:
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1 EPKSCDKTHTCPPCPAPELL.....HEAASPSQTVQRAVSVNPGK 569
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Sequence of human
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AAU80283
ID AAU80283
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32	32	32	32	52	5 ω	53	79	79	60	60	60	60	23	41	31	26	48	69	8	8	77	77	9	89	11	30	15	25	36	25	67	331	5	25
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88	AAY72915		AAW26232	AAW48650	ABB73415			AAW83962	AAB31694	7	28							AAY96531	ABB73412	AAB16959	ABB73418	AAB16967	AAY96779	AAY96780	AAW85692	AAU80289	AAR85582	AAR83582	AAU80288	9	2	036	R7724	AAR75225
IgGgammal h	Human partial IgG1	IgGga		avy chain of		Ø			sequen	A39R s	lia A3	1 A39R s	4-2	HMFG-1	HMFC	1 (120-2	GP-1 (99		TMP-TMP	TMP-TMP	EMP-EMP nuc	MP-EMP prot	1-FD-	-FD-Fc-FD	II fusion p	man IgE C2-C3-C	epsilon) CF	H4 of h		=	_	n IgE heavy c	n IqE Fc chai	Human IgE Fc chain

ALIGNMENTS

FH Key Location/Qualifiers FT Domain 11116 FT Domain /note= "IgE heavy chain C1 domain" FT Domain 113208 FT Negion /note= IgE heavy chain C2 domain FT Region /note= "Epitope including C2C3 linker" FT Region /note= "Igitable decide between C2 and C2 and C315"

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Matches 347
                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful for downregulating and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C1-C2-C3-C4 domains used to create the epitopes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g immune response against autologous immunoglobulin E in an
by effecting simultaneous presentation of cytotoxic T
yte epitope an/or B-cell epitope derived from the immunoglobulin
                                                                                                                                                                                                                                                                                         Similarity
              PSPFDLFTRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                  GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA 304
                                                                                                                                                                                                                   QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTMTLPATTLTL
PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                         -- SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
                                                                                                                                                                SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC---
                                                                                                                                                                                         VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGSGGGGS
                                                                                                                                                                                                                                              REPOVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS
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2000US-232831P
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321..4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "IgE heavy chain C4 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Epitope including C3C4 linker"
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Pred. No. 9.5e-11
7; Mismatches 5
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constant region. The invention is based on the constant domain in the polypeptide that includes the CH1 (i.e. constant domain in the heavy chain) and/or CH4 domain(s) of an IgE molecule, coupled to a carrier, can be used to induce in a mammal the production of antibodies that specifically bind to IgE of the mammal. Compositions are provided for inducing self-specific anti-IgE antibodies. These contain carriers foreign to the immunised mammal coupled to polypeptides containing fragments of the IgE molecule, especially fragments including the constant CH1 and/or CH4 domain, but not the CH3 domain. CH1 polypeptides have at least 95% identity to amino acids 1-110, 105, 5-105 or 5-95 of the present sequence, this carriers is a sequence.
                                                                                                                                                                                                                     Composition for treating immunoglobulin (Ig) E-mediated disorder such as anaphylactic shock, allergic rhinitis and conjunctivitis, comprises a polypeptide that includes CHI and/or CH4 domains of IgE molecule coupled to a carrier
                                                                                                                                                                                                                                                                                       WPI;
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(BACH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antianaphylactic;
antiinflammatory;
                                                                                                                                                                                              Claim 41; Page 9; 71pp; English
                                                                                                                                                                                                                                                                                                                Bachmann MF,
                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-2002
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                                                                                                                                                                                                                                                                                                                                         (RENN/)
                                                                                                                                       present sequence is that of the human IgE epsilon chain stant region. The invention is based on the discovery that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin E; antibody; human; allergy; asthma; eczema; anaphylactic shock; allergic rhinitis; conjunctivitis; anaphylactic; immunosuppressive; antiallergic; antiasthmatic; inflammatory; dermatological; vasotropic; ophthalmological;
                                                                                                                                                                                                                                                                                       2002-227076/28
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313..428
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Matches 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eczema or urticaria (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                              Human; immunoadhesin;
human rhinovirus; immu
                                                                                                                                                                                                                                                                                                                             22-FEB-2002
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                   28-APR-2000; 2000US-200298P
                                                         28-APR-2001; 2001WO-US13932
                                                                                               08-NOV-2001
                                                                                                                                WO200183529-A2
                                                                                                                                                                                                            transgenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICRAVHEAASPSQTVQRAVSVNPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
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                                                                                                                                                                                                                                                                                     heavy chain constant region amino acid sequence
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78.0%;
                                                                                                                                                                                                                              intercellular adhesion i
unoglobulin heavy chain;
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Pred. No. 9.5e
17; Mismatches
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).5e-115;
les 57;
                                                                                                                                                                                                                              molecule;
; J chain;
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HRV; co
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VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGSGGGGS

QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTMTLPATTLTL REPOVYTLPPSRDELTKNOVSLT---CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS

Conservative

17;

Score 1766; Pred. No. 9 Mismatches

DB 23;).5e-115; hes 57;

Indels Length

24;

Gaps

SGHYATISLLTV-SGAWAK-OMFTCRVAHTPSSTDWVDNKTFSVC------

GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA--SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA

163 304 105 244 62 185

ICRAVHEAASPSQTVQRAVSVNPGK

ICRAVHEAASPSQTVQRAVSVNPGK

ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST PSPEDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST ${\tt STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR}$ STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR

484

283

424 223 364

ACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF

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reducing infection by human rhinovirus (HRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and reduces its infectivity, competing with cell surface ICAM-1 for binding sites, interfering with virus entry or uncoating and directing premature release of viral RNA and formation of empty capsids. Expression of the immunoadhesin in plants would be tetrameric, rather than dimeric. Immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectiveness of the immunoadhesin. Association of secretory component and immunoglobulin J chain increases the stability of the immunoadhesin in the mucosal environment. Production is significantly less expensive in plants than in animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a human immunoglobulin protein sequence, useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising: rithinovirus receptor protein linked to at least a portion of immunoglobulin heavy chain; and (b) optionally a Take of the protein continuation of the protein continuation of the protein and (c) optionally a Take of the protein continuation o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycosylation and virucide activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRV) and hence the initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin heavy chain; and (b) optionally a J chain and secretory component associated with chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 7; 138pp;
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                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLAN-) PLANET BIOTECHNOLOGY
                                                                                                                                                                                                                                                                    428
                                                                                                                                                                                                                                                                    AΑ;
57.7%;
78.0%;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 349
                                                                                                                                                                                                                                                                                                                                               DNA encoding IgE H-chain and frags. is claimed (AAN40062). Transformant conto. the DNA is also new, esp. Escherichia coli IFO-14284, -5 and -6. The transformant may be grown to produce a polypeptide of immunological or biological activity equivalent to that of the human IgE H chain. AAN40062 or frags. is pref. linked at site downstream from a promoter, e.g. rec A promoter (see AAN40064)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide having activity of human immunoglobulin from host transformed with recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP102634-A.
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kikuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-SEP-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP40065 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TAKE ) TAKEDA CHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-1992
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                                                                                                                                                                                                                                                                                            Similarity
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GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWP
            GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWP
                                            GVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRN
                                                        GVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRN
                                                                                                       MDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPR
                                                                                                                                                    GGSGGGGSGTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQV
                                                                                                                                                                                                        TTP-PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of human
                                                                                                                                                                                    TLPATTLTLSGHYATISLLTV-SGAWAK-QIFTCRVAHTPSSTDWVDNXTF---
                                                                                                                                                                                                                                 TVSSASTQ--SPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTM
                                                                                                                                                                                                                                                        TISKAKVQPREPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYK 177
                                                                                           MDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPR
                                                                                                                                        -----SVCSRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQV
                                                                                                                                                                                                                                                                                                                            493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               Fig 2; 61pp; English.
                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83EP-0108699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    suppressor;
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                                                                                                                                                                                                                                                                                          57.5%;
77.0%;
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                                                                                                                                                                                                                                                                                14;
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                                                                                                                                                                                                                                                                             Score 1760; DB 5;
Pred. No. 3e-114;
4; Mismatches 66;
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                                                                                                                                                                                                                                                                                                       493;
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RESULT 5
AAU80287
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     Inducing immune response against autologous immunoglobulin {\tt E} in animal, by effecting simultaneous presentation of cytotoxic {\tt T}
                           WPI;
                                                                      06-SEP-2000;
15-SEP-2000;
                                                                                           06-SEP-2001; 2001WO-DK00579
                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                             Synthetic
                                          Klysner
                                                        (PHAR-) PHARMEXA AS
                                                                                                           14-MAR-2002.
                                                                                                                         WO200220038-A2
                                                                                                                                               Domain
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                                                                                                                                                                                                                                                                                                                                                                  heavy
                                                                                                                                                                                                                                                                                                                                                                                IgE; allergy;
antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU80287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU80287
                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                      Human IgE heavy chain C1-C2-C3-C4 domains with MIGIS fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                          vaccine;
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                                                                                                                                                                                                                                                                                                                                                    sapiens
                           2002-383033/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461
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                                                                                                                                                                                                                                                                                                                                                                  chain
                                          s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anaphylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EWEOKDEFICPAVHEAASPSOTVORAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK
                                         Von Hoegen
                                                                      2000DK-0001326.
2000US-232831P.
                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                  ; dermatological; antiinflammatory; immunog
hylaxis; allergic rhinitis; asthma; atopic
domain; MIGIS.
                                                                                                                                                                                                                                                                                                                                                                                        human;
                                                                                                                                            321..422
/note= "IgE heavy chain
                                                                                                                                                                          /note=
318..3
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                                                                                                                                                                                                                                                                                                         /note=
113..2
                                                                                                                                                                                                                     272..280
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 11..106
                                                                                                                                                                                         315..323
                                                                                                                                                                                                       301..311
                                                                                                                                                                                                                                    244..251
                                                                                                                                                                                                                                                                217..317
                                                                                                                                                                                                                                                                              209..216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
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                                                                                                                                                                                                                                                                                                          . 208
                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                       antiallergic;
                                          ٦,
                                                                                                                                       "MIGIS fragment"
                                                                                                                                                                   "Linker
                                                                                                                                                                                "Epitope including C3C4
                                                                                                                                                                                                "Epitope
                                                                                                                                                                                                                           "Epitope
                                                                                                                                                                                                                                                       "IgE heavy chain C3
                                                                                                                                                                                                                                                                                    "Epitope including C2C3 linker"
                                                                                                                                                                                                                                                                                                                "IgE heavy
                                                                                                                                                                                                              "Epitope
                                                                                                                                                                                                                                         "Epitope
                                                                                                                                                                                                                                                                     "Linker
                                                                                                                                                                                                                                                                                                  IgE heavy chain
                                         Voldborg
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linflammatory; immunoglobulin E; IgE;
                                          В,
                                                                                                                                                                                                loop"
                                                                                                                                                                                                                            loop"
                                                                                                                                                                                                                                          Toop"
                                                                                                                                                                                                                                                                      between C2 and
                                                                                                                                                     C4
                                                                                                                                                                                                                                                                                                   C2
                                                                                                                                                                                                                                                                                                                CI
                                          Gautam
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                                                                                                                                                     domain"
                                                                                                                                                                                                                                                        domain"
                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493
                                                                                                                                                                   C
                                                                                                                                                                                  linker"
                                                                                                                                                                   andC4"
                                                                                                                                                                                                                                                                       C
                                                                                                                                                                                                                                                                     region"
                                                                                                                                                                                                                                                                                                                                                                         dermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460
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lymphocyte

epitope an/or

B-cell

epitope

derived

from

the

immunoglobulin

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RESULT 6
AAR42950
ID AAR4
XX
AC AAR4
XX
DT 12-P
XX
DE Huma
XX
KW Immu
KW ECR
KW tarc
XX
OS Homc

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                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E [IgB] in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic crhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain CI-C2-C3-C4 domains fused to the MIGIS of fragment used to create the epitopes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 345
                                                                       Human IgE heavy chain constant region (residues 120-547).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                  Immunoglobulin E; IgE;
FCR region; allergen; a
                                                                                                12-MAY-1994
                                                                                                                                               AAR42950 standard;
                                                                                                                                                                                                                                                          344
                                                                                                                                                                                                                                                                                  485
                                                                                                                                                                                                                                                                                                         284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 REPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS
                                                                                                                                                                                                           404
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                                                                                                                                                                                                                                                                                                                                                                                                                    STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEGGGGSGGGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTMTLPATTLTL
                                                                                                                                                                                                                       ICRAVHEAASPSQTVQRAVSVNP 567
                                                                                                                                                                                                                                                         ACLIQNEMPEDISVQMLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                                                                                                                                                                                                  ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                                                                                                                                                                                                                                     LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                                                                                                                                                                                                                                                     PSPFDLF IRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                                                                                                                                                                                                                                                                                                                      STTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC--
                                                                                                                                                                                                                                                                                                        LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                                                                                                                                                                                                                                                                         PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                     --SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA
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                                                                                                (first
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                                                                                                                                              protein;
                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.48;
77.98;
                                    allergic
                                   epsilon heavy chain; IgE receptor binding;
allergic reaction; catalytic antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                               428
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Pred. No. 5
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                                                                                                                                               B
                                                                                                                                                                                                           426
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5.7e-114;
hes 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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Query Match
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Catalytic antibodies which cleave specific target sequences in the IgE heavy chain constant region are exemplified. Cleavage is targetted so as to separate the Fab (antigen binding region) from the Fc region (contg. FcR binding site for attachment to the IgE receptor on mast cells), thereby destroying receptor binding activity. The target peptides were selected after consideration of their primary and secondary structure. The antibodies can be used to block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Selecting catalytic antibodies which cleave target peptide - to block allergic reactions or as preventive treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davis CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-SEP-1990;
22-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5258289-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 3; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DAVI/) DAVIS
                                                                                                                426
                                                                                                                                                                                                                                                                                                          105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 REPQYYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYKTTP-PVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345;
                                                                                                                                                                                                                                                                                                                                                                                 63
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QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTMTLPATTLTL
                                                                             PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATREWPGSRDKRTLA
                                                                                              PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLA
                                                                                                                                                    SPEDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                        SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                               TTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSATLSRP
                                                                                                                                                                                                                                                     TTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRP
                                                                                                                                                                                                                                                                                                                                                                                 SGHYATISLLTV-SGAWAK-QMFTCRVAH-----TPSSTDWVDNKTE-----SV
                                                                                                                                                                                                                                                                                                                                                                                                                     VGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGGSGGGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fabian GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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91US-0780765
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193..22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= FcR_binding_region
/note= "residues 301-376 of IgE H chain,
/note= in binding to IgE receptors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 181..257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.3%;
77.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1723;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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RESULT 7
AAU80284
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                 This invention relates to a novel method for inducing an immune resagainst autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphc (CTL) epitope and/or B-cell epitope derived from IgE, and T helper epitope (TH epitope) which is foreign to the animal, by antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rgk; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
heavy chain C domain.
  presenting
                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-2001;
                                                                                                                                                                                                        Inducing immune response against autologous immunoglobulin E in animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
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                                                                                                                                                Page 105-106;
                                                                                                                                                                                                                                                                                                                                      Von
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2000US-232831P
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210..2
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104..111
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216..3
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167..1
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112..2
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196..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
    (APCs) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
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                                                                                                                                                                                                                                                                                                                                      P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "IgE heavy chain C4 domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Epitope including C3C4 linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Epitope
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    the animal's
                                                                                                                                                                                                                                                                                                                                      Voldborg
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                                                                                                                                                                                                           the immunoglobulin
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                                                                                                     immune response
                                                            Lymphocyte
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system.

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WPI; 2002-383033/41 N-PSDB; ABK51133.

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RESULT 8
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Best Local s
Matches 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains used to create the epitopes of the invention.
                                                                                    06-SEP-2000;
15-SEP-2000;
                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
                                                                                                                                                                                                                                                                                                                          30-JUL-2002
                                                                                                                        06-SEP-2001;
                                                                                                                                                 14-MAR-2002
                                                                                                                                                                          WO200220038-A2
                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                    AAU80285;
                                                                                                                                                                                                                                                                                                                                                                           AAU80285 standard;
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                                                                                                                                                                                                                                     ne; anaphylaxis; allergic rhinitis;
chain C domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                        304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124
                                                                                                                                                                                                                                                                                                  IgE C2-C3-C4 domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
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                                   s,
                                                           PHARMEXA AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                        HEAASPSQTVQRAVSVNPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
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                                   Von Hoegen
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                                                                                   2000DK-0001326.
2000US-232831P.
                                                                                                                        2001WO-DK00579
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                                                                                                                                                                                                                                                                                                                        entry)
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                                   ָש,
                                   Voldborg B,
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Pred. No. 8.4e-111;
0; Mismatches 0;
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matic; dermatological; antiinflammatory; immunoglobulin E; Iç
anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              animal, by lymphocyte
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15-SEP-2000;
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Pred. No. 8.4e-111;
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RESULT 10 AAR83559 ID AAR83

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;
constant heavy region; E.coli; glycosylation; antigenic; immunogenic;
histamine; anti-allergenic; vaccine; immune response.
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                                                                                                                                                                                              FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
              RDWIEGETYQCRVTHPHLPRALMRSTIKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                 324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Panero MJM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH2'.-CH4 protein
                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                       55.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      French
                                                                                                                                                                                                                                       Score 1707; DB 16; Pred. No. 8.5e-111;
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                                                                                                                                                                                                                                                     324;
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RESULT 11
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             The sequence chain (amino Fc-epsilon R cells. The
                                                   Disclosure; Page 6;
                                                                 Mutated glycosylated polypeptide(s) useful to study and treat allergy.
                                                                                                WPI; 1995-206936/27
                                                                                                               Gould HJ,
                                                                                                                            (THRE-) 3I RES EXPL LTD. (CLLT ) CELLTECH THERAPEUTICS
                                                                                                                                                   22-NOV-1993;
                                                                                                                                                                  22-NOV-1994;
                                                                                                                                                                                                W09514779-A
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                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                     Human IgE Fc
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                                                                                                                                                                                                                                                                                                                                                                                                       IgE Fc fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR75225;
              sequence represents a mutant sequence of a human IgE-F in (amino acids 224-547) which is of sufficient length epsilon RI and/or Fc-epsilon FII IgE receptor sites on is. The protein is useful in the study and treatment o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305
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                                                                                         AAQ87474.
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                                                                                                               Owens
                                                                                                                                                                                                                                                                                                                                                                                                                    chain (amino acids 224-547) mutant sequence
                                                                                                                                                    93GB-0024013
                                                                                                                                                                  94WO-GB02561
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172
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                                                                         of human
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allergy

to bind

IgE-Fc to bind

0; Gaps

309 65

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RESULT 12
AAR77241
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XX AAR77
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XX IGE Human
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OS Homo
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XX Homo
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Best Local :
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                                                                                                                                    Gould HJ,
                                                                                                                                                                                                                                                                                       01-JUN-1995
                                                                                                                                                                                                                                                                                                                      W09514779-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IgE Fc fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human IgE Fc chain (amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR77241 standard; Protein; 325
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   Disclosure;
                                 Mutated glycosylated polypeptide(s) contg. useful to study and treat allergy.
                                                                                   WPI; 1995-206936/27
N-PSDB; AAQ91170.
                                                                                                                                                                                                                                                     22-NOV-1994;
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                                                                                                                                                                                                                    22-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEAASPSQTVQRAVSVNPGK 325
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                                                                                                                                  Owens RJ,
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Page 35-36;
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172
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                                                                                                                                    Sutton
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55pp; English.
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Best Local S
Matches 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents the wild-type sequence of a human IgE-Fc chain (amino acids 224-547) which is of sufficient length to bind Fc-epsilon RI and/or Fc-epsilon FII IgE receptor sites on human cells. The sequence is preferably mutated (see AAR75225) to represent a protein encoding a protein where Cys225 is mutated, optionally together with Val224, Ser226 and Arg227. The protein is useful in the study and treatment of allergy.
                                                                                                                                                                                                                                                  11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                WPI; 2000-365342/31
                                                                                                                                                                   02-NOV-1998;
22-SEP-1999;
                                                                                                                                                                                                                    21-OCT-1999;
                                                                                                                                                                                                                                                                                   WO200025722-A2
                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     asthma; eczema;
                                                                                                                                                                                                                                                                                                                                                                     Human; immunoglobulin E;
                                                                                                                                                                                                                                                                                                                                                                                                     Human IgE heavy chain constant regions
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                                                                                                                                  (RESI-) RESISTENTIA PHARM AB
               Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEAASPSQTVQRAVSVNPGK 569
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                                                                                                                                                                  98US-0106652.
99US-0401636.
                                                                                                                                                                                                                    99WO-SE01896.
                                                                                                                                                                                                                                                                                                                                                     immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                     IgE; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1707; DB 16; pred. No. 8.5e-111;
                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      ۷,
                                                                                                                                                                                                                                                                                                                                                                                                        ω
                                                                                                                                                                                                                                                                                                                                                                     infection; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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549

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489

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RESULT 14
AAP80291
ID AAP80
XX AAP80
AC AAP80
AAP80
AC AAP80
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SXSSSSSSSSSSXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 320
                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2, 3 and 4 of the human IgE. It was used to construct a number of immunogenic peptides which consisted of regions of IgE from different mammals, which appear to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.
                                                                                                     EP269455-A.
                                                                                                                                                                                                                                                                                               synthetic
 18-SEP-1987;
                                  27-NOV-1987;
                                                                    01-JUN-1988
                                                                                                                                         Peptide
                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                 Interleukin-2;
                                                                                                                                                                                                                                                                                                                                                                  Interleukin-2/IgE Fc
                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP80291 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEAASPSQTVQRAVSVNPGK 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.8%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                 IgE
 87JP-0232295
                                  87EP-0310475
                                                                                                                                     /label
37..36
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                                                                                                                                                                                                                            /label=IL-2 leader sequence
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                          'label-IL-2 N-terminal
                                                                                                                                                                                                                                                                                                                                 Fc receptor; fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                  fusion protein
                                                                                                                                                         _=linker
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Pred. No. 8.7e-111;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                 protein; asthma; dermatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
20-JUN-1998;
                                21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430
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Query Match
Best Local Similarity
Matches 320; Conserv
                                                                                                        anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis;
                                                                                                                           Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
immunogenic; immunostimulatory; carrier protein; helper T cell ep
antibody; allergy; allergic disease; immunisation; anti-allergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-terminal
29-DEC-1999
                                    WO9967293-A1
                                                                                                                                                                                                   Human immunoglobulin E epsilon heavy chain SEQ ID
                                                                                                                                                                                                                                         15-MAY-2000
                                                                                                                                                                                                                                                                                                               AAY79994 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fused protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1988-149211/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s fusion protein has a low toxicity and is useful in therapy allergy induced by IgE. It can be used in the treatment of ergic dermatosis, atopic dermatitis or bronchial asthma.
                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sin for allergy treatment - comprising interleukin-2
residues, a linker and human immunoglobulin E Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.8%; Score 1707; DB 9; llarity 100.0%; Pred. No. 9.9e-111; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishimura
                                                                                                                                                                                                                                       (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                       entry)
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                                                                                                          dermatitis
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99WO-US13959 98US-0100287

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                                                                                                                                                                                                                                                                                                                                                                                      Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes immunoglobulin E (IgE)-CH3 domain CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic CC and anti-asthmatic properties. (I) induces polyclonal antibodies Specific for a target effector site on the ppsilon-heavy chain of IgE, CC and so preventing triggering and activation of mast cells and basophils CC and downregulation of IgE synthesis. Conjugates, or fusion peptides, CC containing (I) are used for active immunisation against IgE-mediated CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy CC dermatitis. Nucleic acids that encode these compounds are useful for CC recombinant production of corresponding peptides or in DNA vaccines. CC Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell CC constraints (disulfide bridge) to stabilise conformational features and CC maximize cross-reactivity to the natural target. They induce safe CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.6
Best Local Similarity 99.4
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-160578/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 66-68; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antigenic peptide from the CH3 domain of immunoglobulin {\tt E}, fusions for immunization against allergy -
490
                                                                                                                                                                             430
                                                                                                                                                                                                              126
                                                                                                                                                                                                                                                370
                                                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                          186
                                                                                                                                                                                                                                                                                                                    310
                                                                                                                                                                                                                                                                                 66
                                                                                                                                                                                                        LFIRKSPTITCLVVDLAPSKGTVNLIWSRASGKPVNHSTRKEEKQRNGTLIVTSTLPVGT 429
                                                                                                                                                                                                                                                                               GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                       NEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV 549
                                                                                                                                                           RDWIEGETYQCRVTHPHLPRALMRSTIKTSGPRAAPEVYAFAIPEWPGSRDKRTLACLIQ
                                                                     NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWQEKDEFICRAV 305
                                                                                                                                        RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           55.6%;
99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1701; DB 21;
Pred. No. 2.2e-110;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 325;
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                                                                                                                                          245
                                                                                                                                                                           489
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Search completed: July 15, 2003, 06:57:41 Job time: 68.0009 secs

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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1707
1705.5
1696
1671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US/NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US/NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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length: 2000000000
   US-09-847-208B-7
3060
                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445758 seqs, 116419773 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      July 15, 2003, 06:59:40; Search time 43.6521 Seconds
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : /cgn2_6/ptodata/1/pubpaa/US07_FUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
0: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                           Length DB
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   US-09-847-208-7
US-10-214-524-35
US-10-214-524-35
US-09-847-208-5
US-09-949-375A-1
0 US-09-949-375A-2
US-09-949-375A-2
US-09-949-375A-2
US-09-949-375A-6
US-09-949-375A-6
US-09-949-375A-6
US-09-949-375A-6
US-09-949-375A-6
US-09-949-375A-6
US-09-949-375A-6
US-10-216-656-1
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1517.518 Million cell updates/sec
               Sequence 7, Appli
Sequence 45, Appli
Sequence 37, Appli
Sequence 5, Appli
Sequence 60, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 20, Appli
Sequence 26, Appli
Sequence 39, Appli
Sequence 32, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 37, Appli
Sequence 38, Appli
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 Sequence 8,
Sequence 10,
                           ice 1, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	$\frac{\omega}{\omega}$	32	31	30	29	28	27	26	25	24	23	22	21	20
1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1225	1227	1232	1234.5	1234.5	1260	1260	1273.5	1364.5		1566.5	1579	1649
40.0	40.0	40.0	40.0	•	•	40.0	•	•	40.0		40.0	40.0	40.0	40.1	40.3	40.3	40.3	41.2	41.2			σ	1	51.6	53.9
3 3 2	331	330	330	330	330	288	288	267	251	251	247	235	232	543	660	741	731	330	232	711	346	346	348	347	347
9	9	9	9	9	9	9	9	10	9	9	10	9	10	9	9	10	10	9	9	9	φ	ø	9	9	9
US-09-990-586-98	US-10-341-836-2	US-10-269-805-68	US-09-892-949-38	US-09-995-898A-15	US-10-047-542-20	US-10-119-637A-14	US-09-822-851B-14	US-09-996-357-12	US-10-152-363A-6	US-10-008-063-18	US-09-996-357-13	US-10-207-655-208	US-09-996-357-10	US-10-207-655-345	US-10-294-055-8	US-09-825-012-55	US-09-825-012-46	US-09-847-208-2	US-09-847-208-3	US-10-071-485-90	US-10-152-190-14	US-10-152-190-10	US-10-152-190-11	US-10-152-190-12	US-10-152-190-13
Sequence 98, Appl	Sequence 2, Appli	68,	•	•		Sequence 14, Appl	~	Sequence 12, Appl	74	Sequence 18, Appl	Sequence 13, Appl	Sequence 208, App	Sequence 10, Appl	Sequence 345, App	Sequence 8, Appli	Sequence 55, Appl	Sequence 46, Appl	Sequence 2, Appli	Sequence 3, Appli	Sequence 90, Appl	Sequence 14, Appl	Sequence 10, Appl	11,	Sequence 12, Appl	Sequence 13, Appl

ALIGNMENTS

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APPLICANT: SAXON, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
FITTLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: GUIDANTED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT ETLING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOSTMARE: FRASLER for Windows Version 4.0
SEQ ID NO 7
LENGTH: 569
TUPN: DEFM
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4; OTHER INFORMATION: (IgE) US-09-847-208-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-09-847-208-7
                                                                  В
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09847208 Publication No. US20030082190A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                          121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                       181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGGSG
                                                                                                                                                                                     61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                          61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                     1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                  ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
100.0%; Score 3060; DB 9; 100.0%; Pred. No. 8.5e-181;
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240

180 120

480

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APPLICANT: WYCOFF, KEITH L.

TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
CURRENT FILING DATE: 2001-10-26
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR TILING DATE: 2001-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 45
LENGTH: 574
TYPE: ppm
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; ORGANISM: Homo sapiens
US-10-047-542-45
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US-10-047-542-45
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Best Local
                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                  356
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                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                            120 TISKAKVQPREPQVYTLPPSRDELTKNQVSLT--CLVKGFYPSDIAVEWESNGQPENNYK
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 RGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR
                                                                VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNP
                                                                                                                                                GGGSGGGGGGGFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQ 295
                                                                                                                                                                               TLPATTLTLSGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC-----
                                                                                                                                                                                                             TTP-PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEG
                                                                                                                                                                                                                                                 TVSSASTQ--SPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGSGGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDGGGSGGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVD
                                                 VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGGSG
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                 58.0%;
77.3%;
                                                                                                                 -SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQ
                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                 Score 1775; DB 9; Pred. No. 1.1e-101;
                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                Length 574;
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PRIOR FILING DATE: 2001-08-13
NUMBER OF SEO ID NOS: 61
SOFTWARE: PatentIn version 3.1
SEO ID NO 37
LENGTH: 574
TYPE: PRT
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; Sequence 37, Applica
; Publication No. US20
; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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FILE REFERENCE: IGE-00101.P.1.1

CURRENT APPLICATION NUMBER: US/10/214,524

CURRENT FILING DATE: 2002-08-08

CURRENT FILING DATE: 60/312,120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chen, Zhong
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
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                                                                               PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR
                                                                                                                                                                                                                                                                              VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNP
                                                                                                                                                                                                                                                                                                                                              GGGSGGGGSGTTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQ 295
                                                                                                                                                                                                                                                                                                                                                                                                                             TTP-PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY-QQRSLSLSPGKVEG
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AEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK
                              AEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 569
                                                                                                                                                NGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW
                                                                                                                                                                                                                                                               VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNP
                                                                PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR
                                                                                                                                                                                              RGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR
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                                                                                                                                                                                                                                                                                                                             -----SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQ
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No. US20030073142A1
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77.3%;
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Pred. No. 1.1e-101;
7; Mismatches 60;
574
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355 360

Length 428; Indels

24;

Gaps

62

223

283

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US-10-047-542-60

; Sequence 60, Application US/10047542
; Patent No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; APPLICANT: MYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING ANT TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; CURRENT FILING DATE: 2001-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo s
US-09-847-208-5
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APPLICANT: Zhu, Daocheng
APPLICANT: Zhu, Daocheng
APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09847208
Publication No. US20030082190A1
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
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Best Local Similarity
Matches 347; Conserv
APPLICATION
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NUMBER:
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78.0%;
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Pred. No. 2.8e-101;
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                                                                              AND PREVENTING
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                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09949375A Patent No. US20020172673A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 78.0%; Pred. No. 2.8e-101; Matches 347; Conservative 17: Miamatone.
                                                                                                                                                                                           APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 428
TYPE: PRT
          FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (209)..(216)
OTHER INFORMATION: Linker
                                                                                           FEATURE:
NAME/KEY: DOMAIN
LOCATION: (11)..(116)
                                                                                                                                                             LENGTH: 428
TYPE: PRT
                                                                              OTHER INFORMATION: Human
                                                                                                                                          ORGANISM: homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA 304
--SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ICRAVHEAASPSQTVQRAVSVNPGK 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC------ 105
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; LOCATION: (113)..(208)
; OTHER INFORMATION: Human IgE heavy chain
US-09-949-375A-1
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Best Local
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NAME/KEY: MISC_FEATURE
LOCATION: (272)..(280)
OTHER INFORMATION: Epi
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OTHER INFORMATION: Epitope
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LOCATION: (217)..(316)
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al Similarity 78.0%;
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              ICRAVHEAASPSQTVQRAVSVNPGK 569
                                              ACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFEVESRLEVTRAEWEQKDEF 544
                                                                                             LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL
                                                                                                           LPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484
                                                                                                                                              PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST 424
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ICRAVHEAASPSQTVQRAVSVNPGK 428
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US-09-949-375A-7

Sequence 7, Application US/09949375A Patent No. US20020172673A1 GENERAL INFORMATION:

APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111p
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1

SEQ ID

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US-09-916-230-1
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Patent No. US20020146422A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/221,841
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/916,230 CURRENT FILING DATE: 2001-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bachmann, Martin APPLICANT: Renner, Wolfgan
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TYPE: PRT
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al Similarity 78.0%;
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ICRAVHEAASPSQTVQRAVSVNPGK 428
                                                   ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEF
                                                                                                             PSPEDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTST
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               ICRAVHEAASPSQTVQRAVSVNPGK 569
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Pred. No. 2.8e-101;
.7; Mismatches 57;
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; LOCATION: (301)..(311)
; OTHER INFORMATION: Epitope in
US-09-949-375A-7
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LOCATION: (427)..(441)
OTHER INFORMATION: MIG
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LOCATION: (315)..(323)
OTHER_INFORMATION: Epitope
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                                                                       GGGGSFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA 304
--SRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTA 163
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SEQ ID NO 334
LENGTH: 592
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-10-207-655-334
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Best Local (
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CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hayden-Ledbetter, martha S. TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS FILE REFERENCE: 390069.401C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ledbetter, Jeffrey A. APPLICANT: Hayden-Ledbetter, Ma
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               KPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGP
                                                                                                                                  TPGTINITWLEDGQVMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGH
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                                                         TFEDSTKKCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASG
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KPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGP
                                                                        TFEDSTKKCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASG
                                                                                                                  TPGTINITWLEDGQVMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGH
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; Pred. No. 7.7e-99;
15; Mismatches 51.
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Sequence 2, Application US/09949375A
Patent No. US20020172673A1
GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IG:
FILE REFERENCE: 3631-0111P
CUTRENT APPLICATION NUMBER: US/09/949,375A
CUTRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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APPLICANT: SAXON, ANDREW
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
ITITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 320
                                                                                                                                                                     US-09-949-375A-2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE
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Best Local Similarity
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NAME/KEY: MISC_FEATURE
LOCATION: (100)..(114)
OTHER INFORMATION: Epito
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FEATURE:
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LOCATION: (210)..(218)
OTHER INFORMATION: Epitope
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LOCATION: (216)..(317)
OTHER INFORMATION: Hum
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                             HEAASPSQTVQRAVSVNPGK 569
                                                                                        NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
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; Pred. No. 8.9e-98;
0; Mismatches 0;
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; FEATURE:
; OTHER INFORMATION: Artificial amino acid sequence
US-09-949-375A-4
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                                                     ; OTHER INFORMATION: US-09-949-375A-6
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APPLICANT: KLYSNER, Steen et al.
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                     Sequence 6, Application US/09949375A Patent No. US20020172673A1
GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING
FILE REFERENCE: 3631-0111P
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                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
DEED: 1323
 Best Local Similarity Matches 320; Conserv
                             Query Match
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Best Local
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ORGANISM: Artificial Sequence
                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                           TYPE: PRT
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FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/176,664
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US/99/401,636
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-111-02
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US-10-176-664-1
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Best Local S
Matches 320
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GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 33
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetically generated proteins
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nes 320; Conserv
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 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
               NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAV
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                                                                   RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ
                                                                                                           LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
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100.0%; Pr
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Pred. No. 9.1e-98;
0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 329
LENGTH: 331
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion polypeptide
US-10-207-655-329
Search completed: July 15, 2003, 07:17:20 Job time: 44.6521 secs
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US-10-207-655-329
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Best Local Similarity 100.0%;
Matches 320; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
                                                            308
                                                                          550 HEAASPSQTVQRAVSVNPGK 569
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                                                            HEAASPSQTVQRAVSVNPGK 327
                                                                                                                    NEMPEDISYOWLHNEYQLPDARHSTTQPRKTKGSGFFYFSRLEYTRAEWEQKDEFICRAY 549
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Pred. No. 9.1e-98;
0; Mismatches 0;
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1: /cgn2_6/ptodata/1.

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    Maximum Match 100%
Listing first 45 summaries
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US-09-459-066-8
US-08-595-043A-50
US-09-178-869-2
US-09-118-1100-11
.US-08-457-918-7
US-08-457-918-7
US-08-457-918-7
US-08-457-918-7
US-08-744-512-3
S-09-176-228-3
PCT-US95-03866-14
PCT-US95-03866-14
PCT-US96-10043-9
US-08-397-411-7
US-08-458-516-13
US-08-458-5110A-7
US-08-487-550-12
US-08-487-550-13
US-08-487-550-13
US-08-487-550-13
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US-08-487-550-3
US-08-284-391B-33
US-09-131-247-3
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US-09-181-706-8
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1219 39.8 451 2 US-08-887-352B-16 1219 39.8 451 3 US-08-466-151-65 1219 39.8 451 4 US-09-109-207C-14 1219 39.8 451 4 US-09-109-207C-16 1219 39.8 451 4 US-09-109-207C-16 1219 39.8 451 4 US-09-109-207C-18 1219 39.8 451 4 US-09-282-505-2 1219 39.8 451 4 US-09-282-505-2 1219 39.8 451 4 US-09-296-005-14 1219 39.8 451 4 US-09-296-005-16 1219 39.8 451 4 US-09-296-005-18 1219 39.8 451 4 US-09-296-005-18 1219 39.8 452 4 US-09-206-985-71 1219 39.8 452 4 US-09-121-952A-71 1219 39.8 453 4 US-09-121-952A-71 1219 39.8 453 4 US-09-2466-153B-8 1219 39.8 453 4 US-08-466-153B-8	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29
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US-08-887-352B-16 US-08-887-352B-18 US-08-466-151-65 US-09-109-207C-14 US-09-109-207C-18 US-09-109-207C-18 US-09-282-505-2 US-09-286-005-18 US-09-296-005-18	4	ω	4	4	4	w	4	4	4	4	4	4	4	4	ω	2	N
	US-08-466-163B-8	US-08-466-151-8	US-09-234-340A-71	US-09-121-952A-71	US-09-026-985-71	US-09-027-449-71	US-09-296-005-18	US-09-296-005-16	US-09-296-005-14	US-09-054-255-2	US-09-282-505-2	US-09-109-207C-18	US-09-109-207C-16	US-09-109-207C-14	-466-151-	80-	US-08-887-352B-16

ALIGNMENTS

US-09-485-737B-90

Sequence 90, Application US/09485737B Patent No. 6350860

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APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/EP 98/05165
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR APPLICATION NUMBER: EPO 97870122.5
                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.0 SEQ ID NO 90 LENGTH: 711
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1997-08-18 NUMBER OF SEQ ID NOS: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                      121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                          236 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                   296 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKT
                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                               1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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Similarity 50.1%; Pred. No. 2.50
86; Conservative 45; Mismatches
                                                                                                                                                                                                                                             NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
  GGGSGGGSFTPPTVKILQSSCD----
                                                               PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGGSG
                                         PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKL-----
                                                                                                                             ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
-GGGHFPPTIQLLCLVSGYTPGTINITWLED---
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US-09-181-706-8
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                                                                                             TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TOPOLOGY: 11
MOLECULE TYPE:
                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (206)470-4189
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: --to be ass
APPLICATION NUMBER: conversion
FILING DATE: October 26, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Melanie K. Spriggs, Michael R. Comeau, APPLICANT: Robert F. DuBose, Richard S. Johnson TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTTITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                               LENGTH: 660 amino acids
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/958,590
APPLICATION NUMBER: Provisional,
FILING DATE: October 28, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: Octobe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHP
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                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                    US 08/958,598 (converted to a
                                                                                                                                                                                                                                                                                                         --to be assigned--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version
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                                                                                                                                                                                                                                                                                                         (USSN 08/958,598
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                                                                                                                                                                                                                                                                                     application)
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US-09-4...
; Sequence 8, App...
; Patent No. 6174689
; GENERAL INFORMATION:
: APPLICANT: Spriggs, Me
: TITLE OF INVENTION: VI
                                                      TOPOLOGY: linear;
;
MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: S
US-09-458-791-8
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 Query Match
Best Local Similarity
Matches 227; Conserv
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Best Local
                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TIFE. FACE COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS/Windows 95 7.0a
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/458,791 FILING DATE: 10-Dec-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/958,598 FILING DATE: 28-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGKVEGGGGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                    LENGTH: 661 amino acids
                                                                                                                                                                                                   TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09458791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKRSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273
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               40.3%;
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VIRAL ENCODED SEMAPHORIN PROTEIN
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                                                                                   SEQ
Score 1232; DB 4;
Pred. No. 7.2e-96;
7; Mismatches 8
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Pred. No. 7.2e-96;
7; Mismatches 8;
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                                                                                   NO:
                                                                                                                                                                                                                                                       2631
                               DB 4;
                                 Length 660;
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                                                                                                           US-09-459-066-8
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US-09-459-066-8
                                                      Best Loc
Matches
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                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Sprigg
                                                                                                                                              TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFFLICANT: Spriggs, Melanie TITLE OF INVENTION: VIRAL ENTITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windov
SOFTWARE: Word for Windows 95,
                                                                                                                                                                                                                                                        NAME: Henry, Janis C REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                       Conservative
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IBM PC compatible
cvertem: MS-DOS/Windows 95
cvertem: 95, 7.0a
                                                                                                                                      linear
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                                                   Score 1232; DB 4;
Pred. No. 7.2e-96;
"vismatches 8;
                                                                              Length 660;
                                                      Indels
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US-08-595-043A-50
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                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 397-83 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: SG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: CARROLL, PETER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UATE: 31-JAN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 31-JA
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                                                                                          NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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                                               ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                             EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                      Conservative
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0 MONTGOMERY STREET,
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97.0%;
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                                                                                                                                                                                                                      Mismatches
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-11
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US-09-180-100-11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-869-2
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US-09-178-869-2
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
                                   Query Match
Best Local Similarity
Matches 225; Conserv
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Best Local
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LENGTH: 331
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                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tao, Weng
APPLICANT: Wong, Shou
APPLICANT: Hickey, William F
APPLICANT: Hammang, Joseph P.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/178,869B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
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                                     Conservative
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                                   Score 1225; E
Pred. No. 1.2e
3; Mismatches
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Best Loc
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                                Query Match
                                                                                                                                                         TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
                                                                                                                       SEQUENCE CHARACTERISTICS: LENGTH: 371 amino acids
                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: 415/225-1896
                                                                                                                                                                                                                                                                                               FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/84 FILING DATE: 18-FEB-1992 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 07/9:
FILING DATE: 26-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
 Local Similarity
les 225; Conserv
                                                                                       LENGTH: 5/1
TYPE: amino acid
                                                                                                                                                                            TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                              NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/2
FILING DATE: 28-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/236,311 FILING DATE: 02-MAY-1994
                                                                                    TOPOLOGY:
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Score 1225; D
Pred. No. 1.2e
3; Mismatches
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                1.2e-95;
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                                            TOPOLOGY: US-08-457-918-7
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   Query Match
Best Local Similarity
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                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
                                                                                                                                                                             REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2:
FILING DATE: 02-MAY-1994
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r: 460 Point San Bruno Blvd
South San Francisco
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                                                                             amino acid
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   Score
Pred.
   No. 1.
   DB 3;
.2e-95;
                 Length 371;
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US-08-784-512-3
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LENGTH: 376
TYPE: PRT
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Sequence 3, Appiron
Sequence 3, Appiron
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Best Local
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Patent No. 6306395
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FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
CURRENT FILING DATE: 1998-11-02
CURRENT FILING DATE: 1998-11-02
                                                                                        GENERAL INFORMATION:
APPLICANT: BARTNI
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                             APPLICANT:
                                                            APPLICANT:
   TITLE
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 ICANT: HUGHES, E OF INVENTION:
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                                                                                                                                   Application US/08784512
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                           BUETTNER, Frank
CATERSON, Bruce
HUGHES, Clare
                                                                           BARTNIK, Eckart
EIDENMUELLER, Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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97.08;
An artificial recombinant substrate (rAGG 1) and native aggrecan to study the proteolytic activity of
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                      181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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                                                                                                   ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 376
                                                                              ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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Pred. No. 1.2e-95;
3; Mismatches 4
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RESULT 12
US-09-176-228-3
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US-08-784-512-3
                                                                                                                                          Sequence 3, Application US/09176228
Patent No. 6180334
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Matches
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                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/
FILING DATE: 17-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 961
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
 APPLICANT: BARTNIK, Eckart
APPLICANT: EIDENNÜELLER, Bernd
APPLICANT: EJETTNER, Frank
APPLICANT: CATERSON, Bruce
APPLICANT: CATERSON, Bruce
TITLE OF INVENTION: and native aggrecan to study the proteolyt
TITLE OF INVENTION: "Aggrecanase" in cell culture systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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nes 225; Conserv
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LECOMMUNICATION THE TRANSPORT NUMBER: 187
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REGISTRATION NUMBER: 33,6
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Suite 500, 3000 K
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(202)672-5399
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PCT-US95-03866-12
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                                                                                                                        Sequence 12, Applicat GENERAL INFORMATION:
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TELEX: 904136
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
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Matches
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                                        APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: LObell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
              NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
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TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 17-JAN-1997
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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97.0%;
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Best Local S
Matches 225
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GENERAL INFORMATION:
APPLICANT: CytoMed, Inc. (all stat
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INFORMATION FOR SEQ ID NO: 12:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                              APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
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TELEFAX: 212-596-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 28-MAR-1994
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MEDIUM TYPE: Floppy
                                                                                                                                                           NUMBER OF SEQUENCES: 3
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Local Similarity 97.0%;
es 225; Conserva+'"~
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REFERENCE/DOCKET NUMBER: CytoMed/2
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                                                                                                     STREET: 1251 Avenue of the Americas CITY: New York
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                                                                       COUNTRY:
                                                                                                                                            ADDRESSEE:
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                                                                                         New York
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                                                                       United States of America
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                            Fish & Neave
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              Floppy disk
                                                                                                                                                                                            FLT-3/FLK-2 LIGAND
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                                                                                                                                                                                                                                                                    (all states except US)
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Pred. No. 1.5e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 424;
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PCT-US96-10043-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application PC/TUS9610043 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
    CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The General Hospital Corporation TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES TITLE OF INVENTION: AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Haley Jr, James F
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          STREET: 2-
STREET: 2-
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish a back-
current: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 28-MAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: P
SOFTWARE: PatentIn
FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                               COUNTRY: . USA
ZIP: 02210-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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97.0%;
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In Release #1.0, Version #1.30
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                                          US 60/000,213
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Pred. No. 1.
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TELERAX: 61//3*.

TELEYAX: 61//3*.

TELEX: 200154

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acids
TYPE: anino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10043-11

40.0%;
97.0%;
Search completed: July 15, 2003, 07:02:42 Job time: 23.8412 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER:
                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                 Gaps
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